

# SEQUENCE LISTING

<110> Bejanin, Stephane  
Tanaka, Hiroaki

<120> HUMAN CDNAS AND PROTEINS AND USES THEREOF

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<141> 2001-08-06

<150> US 60/305,456

<151> 2001-07-13

<150> US 60/302,277

<151> 2001-06-29

<150> US 60/298,698

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Ser	Tyr	Gly	Gly	Lys	Met	Ala	Ala	Gly	Ile	Gly	Leu	Glu	Leu	Tyr	Lys	
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Val	Lys	Arg	Gly	Asn	Thr	Gln	Arg	Leu	Ala	Cys	Leu	Ala	Phe	Ser	Gly	
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 Phe Ala Gly Val Ala Leu Gly Asp Ser Trp Ile Ser Pro Val Asp Ser  
 170 175 180  
 Val Leu Ser Trp Gly Pro Tyr Leu Tyr Ser Met Ser Leu Leu Glu Asp  
 185 190 195  
 Lys Gly Leu Ala Glu Val Ser Lys Val Ala Glu Gln Val Leu Asn Ala  
 200 205 210  
 Val Asn Lys Gly Leu Tyr Arg Glu Ala Thr Glu Leu Trp Gly Lys Ala  
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 Glu Met Ile Ile Glu Gln Val Lys Arg Gly Asn Thr Gln Arg Leu Ala  
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 Met Lys Phe Phe Val Phe Ala Leu Val Leu  
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 gct ctc atg att tcc atg att agc gct gat tca cat gaa aag aga cat 161  
 Ala Leu Met Ile Ser Met Ile Ser Ala Asp Ser His Glu Lys Arg His  
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 cat ggg tat aga aga aaa ttc cat gaa aag cat cat tca tac cat atc 209  
 His Gly Tyr Arg Arg Lys Phe His Glu Lys His His Ser Tyr His Ile  
 10 15 20  
 aca cta cta cca ctt ttt gaa gaa tca tca aag agc aat gca aat gaa 257  
 Thr Leu Leu Pro Leu Phe Glu Glu Ser Ser Lys Ser Asn Ala Asn Glu  
 25 30 35 40  
 aaa cac tat aat tta ctg tat act ctt tgt ttc agg ata ctt gcc ttt 305  
 Lys His Tyr Asn Leu Leu Tyr Thr Leu Cys Phe Arg Ile Leu Ala Phe  
 45 50 55  
 tca att gtc act tgatgatata attgcaattt aaactgttaa gctgtgttca 357  
 Ser Ile Val Thr

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Leu	Gly	Leu	Leu	Met	Leu	Trp	Val	Ser	Gly	Ser	Ser	Gly	Asp	Ile	Val
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Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe
55 60 65
agt ggc agt gga tca ggc aca gat ttc aca ctg aaa atc agt aga gtg 340
Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val
70 75 80
gag gct gag gat gtt ggg gtt tat tac tgc atg caa gct cta caa act 388
Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala Leu Gln Thr
85 90 95 100
cca ttc act ttc ggc cct ggg acc aga gtg gat atc aag cga act gtg 436
Pro Phe Thr Phe Gly Pro Gly Thr Arg Val Asp Ile Lys Arg Thr Val
105 110 115
gct gca cca tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa 484
Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys
120 125 130
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Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg
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Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser
165 170 175 180
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Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys
185 190 195
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Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr
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Lys Ser Phe Asn Arg Gly Glu Cys
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 Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser  
 15 20 25  
 Leu Leu His Val Gln Gly Ser Asn Tyr Leu Asp Trp Tyr His Gln Lys  
 30 35 40  
 Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala  
 45 50 55 60  
 Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe  
 65 70 75





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Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys Pro Asp Gly Ser  
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Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys Ser Thr Ala Arg  
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Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser Phe Ile Cys Asp  
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Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu Ser Cys Glu Ser  
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Pro	Asp	Gly	Ser	Asp	Glu	Glu	Asn	Cys	Thr	Ala	Asn	Pro	Leu	Leu	Cys	
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Asp	Glu	Glu	Asn	Cys	Thr	Ala	Asn	Pro	Leu	Leu	Cys	Ser	Thr	Ala	Arg	
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 gccctcaggc ytcaggcctt cccaggcttg aagattgggc ttcacctggg acctaccctt 240  
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Met Ser Ala Ser Cys Cys Leu Ser Trp Cys Pro Ala

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 Ile His Cys Ile Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys  
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ccc gat ggc agc gat gaa gag aac tgc aca gca aac cct ctg ctt tgc 433  
 Pro Asp Gly Ser Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys  
 35 40 45

tcc acc gcc cgc tac cac tgc aag aac ggc ctc tgt att gac aag agc 481  
 Ser Thr Ala Arg Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser  
 50 55 60

ttc atc tgc gat gga cag aat aac tgt caa gac aac agt gat gag gaa 529  
 Phe Ile Cys Asp Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu  
 65 70 75

agc tgt gaa agt tct caa gct att ttt cca caa att act gtg tcc 574  
 Ser Cys Glu Ser Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser  
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Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser Phe Ile Cys Asp  
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 Val Leu Glu Ala Leu Glu Leu Tyr Asn Lys Leu Val Asn Glu Ala Pro  
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 Val Tyr Ser Val Tyr Ser Lys Leu His Pro Pro Ala His Tyr Pro Pro  
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 Ala Ser Ser Gly Val Pro Met Gln Thr Tyr Pro Val Gln Ser His Gly  
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 Asn Val Asn Ser Ser Val Thr Ala Gln Pro Ala Gln Thr Ser Tyr Leu  
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 Ser Thr Gly Gln Asp Thr Val Ser Asn Pro Thr Tyr Met Asn Gln Asn  
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 Ser Asn Leu Gln Ser Ala Thr Gly Thr Thr Ala Tyr Thr Gln Gln Met  
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 Gly Met Ser Val Asp Met Ser Ser Tyr Gln Asn Thr Thr Ser Asn Leu  
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                                         Met Arg
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Val Ala Glu Asn Pro Cys Gln Asn His His Cys Lys His Gly Lys Val
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Cys Glu Leu Asp Glu Asn Asn Thr Pro Met Cys Val Cys Gln Asp Pro
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Thr Ser Cys Pro Ala Pro Ile Gly Glu Phe Glu Lys Val Cys Ser Asn
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Asp Asn Lys Thr Phe Asp Ser Ser Cys His Phe Phe Ala Thr Lys Cys
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Thr Leu Glu Gly Thr Lys Lys Gly His Lys Leu His Leu Asp Tyr Ile
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Gly Pro Cys Lys Tyr Ile Pro Pro Cys Leu Asp Ser Glu Leu Thr Glu
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Phe Pro Leu Arg Met Arg Asp Trp Leu Lys Asn Val Leu Val Thr Leu
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Tyr Glu Arg Asp Glu Asp Asn Asn Leu Leu Thr Glu Lys Gln Lys Leu
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Arg Val Lys Lys Ile His Glu Asn Glu Lys Arg Leu Glu Ala Gly Asp
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His Pro Val Glu Leu Leu Ala Arg Asp Cys Gln Ala Val Ser Ala Arg
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	65	70
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Lys Cys Thr Leu Glu Gly Thr Lys Lys Gly His Lys Leu His Leu Asp		110
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Tyr Ile Gly Pro Cys Lys Tyr Ile Pro Pro Cys Leu Asp Ser Glu Leu		125
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 Tyr Asp Tyr Gly Thr Asp Asn Phe Glu Glu Ser Ile Phe Ser Gln Asp  
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 Tyr Glu Asp Lys Tyr Leu Asp Gly Lys Asn Ile Lys Glu Lys Glu Thr  
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Leu	Leu	Cys	Val	Cys	Leu	Ser	Gly	Ser	Val	Tyr	Cys	Glu	Glu	Val	Asp	
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Arg	Phe	Asn	Lys	Ile	Lys	Lys	Leu	Thr	Ala	Lys	Asp	Phe	Ala	Asp	Ile	
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Glu	Asp	Gly	Thr	Phe	Ser	Lys	Leu	Ser	Leu	Leu	Glu	Glu	Leu	Ser	Leu	
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Ala	Glu	Asn	Gln	Leu	Leu	Lys	Leu	Pro	Val	Leu	Pro	Pro	Lys	Leu	Thr	
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Leu	Phe	Asn	Ala	Lys	Tyr	Asn	Lys	Ile	Lys	Ser	Arg	Gly	Ile	Lys	Ala	
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Asn	Ala	Phe	Lys	Lys	Leu	Asn	Asn	Leu	Thr	Phe	Leu	Tyr	Leu	Asp	His	
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Cys	Lys	Ala	Asn	Asp	Thr	Ser	Tyr	Ile	Arg	Asp	Arg	Ile	Glu	Glu	Ile	
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cgc	ctg	gag	ggc	aat	cca	atc	gtc	ctg	gga	aag	cat	cca	aac	agt	ttt	984
Arg	Leu	Glu	Gly	Asn	Pro	Ile	Val	Leu	Gly	Lys	His	Pro	Asn	Ser	Phe	
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 Asn Gln Leu Leu Lys Leu Pro Val Leu Pro Pro Lys Leu Thr Leu Phe  
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 Ala Asn Asp Thr Ser Tyr Ile Arg Asp Arg Ile Glu Glu Ile Arg Leu  
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 Glu Gly Asn Pro Ile Val Leu Gly Lys His Pro Asn Ser Phe Ile Cys  
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ccc tac acc cag ggc aag tgg gaa ggg gag ctg ggc acc gac ctg gta	147
Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp Leu Val	
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Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro Asn Leu	
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Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile Asp His	
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Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg Glu Trp	
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Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln Asp Leu	
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Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala Ala Val	
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Pro	His	Gln	Thr	Ile	Tyr	Ser	Ala	Leu	Met	Ile	Arg	Ser	Glu	Asp	Ala
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Phe	Leu	Pro	Gly	Met	Asn	Pro	Pro	Pro	Tyr	Ser	Gln	Phe	Leu	Ser	Arg
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Leu	Lys	Pro	Arg	Ala	Arg	Met	Thr	Pro	Ala	Pro	Ala	Ser	Cys	Ser	Gln
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Gly	Val	Val	Arg	Gly	Gly	Arg	Val	Asn	Thr	His	Ala	Gly	Gly	Thr	Gly
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 Met  
 1  
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 Arg Leu Arg Ala Gln Val Arg Leu Leu Glu Thr Arg Val Lys Gln Gln





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 <223> Xaa = Asn,Thr

<220>  
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 Gln Tyr Ala Asp Cys Ser Glu Ile Phe Asn Asp Gly Tyr Lys Leu Ser  
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 Gly Phe Tyr Lys Ile Lys Pro Leu Gln Ser Pro Ala Glu Phe Ser Val  
 65 70 75 80  
 Tyr Cys Asp Met Ser Asp Gly Gly Gly Trp Thr Val Ile Gln Arg Arg  
 85 90 95  
 Ser Asp Gly Ser Glu Asn Phe Asn Arg Gly Trp Lys Asp Tyr Glu Asn  
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 Gly Phe Gly Xaa Phe Val Gln Lys His Gly Glu Tyr Trp Leu Gly Asn  
 115 120 125  
 Lys Asn Leu His Phe Leu Thr Thr Gln Glu Asp Tyr Thr Leu Lys Ile  
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 Asp Leu Ala Asp Phe Glu Lys Asn Ser Arg Tyr Ala Gln Tyr Lys Asn  
 145 150 155 160  
 Phe Lys Val Gly Asp Glu Lys Asn Phe Tyr Glu Leu Asn Ile Gly Glu  
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 Tyr Ser Gly Thr Ala Gly Asp Ser Leu Ala Gly Asn Phe His Pro Glu  
 180 185 190  
 Val Gln Trp Trp Ala Ser His Gln Arg Met Lys Phe Ser Thr Trp Asp  
 195 200 205  
 Arg Asp His Asp Asn Tyr Glu Gly Asn Cys Ala Glu Glu Asp Gln Ser  
 210 215 220  
 Gly Trp Trp Phe Asn Arg Cys His Xaa Ala Asn Leu Asn Gly Val Tyr  
 225 230 235 240  
 Tyr Ser Gly Pro Tyr Thr Ala Lys Thr Asp Asn Gly Ile Val Trp Tyr  
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tggaacaaa ggaatagtct gcctggaatc cctgcagatc ttggggccgg aggccagtcc 180
aacccttgga gcaggaagaa acgcaaagtt gtcaagaacc aagtcgagct gcctcagagc 240
cgcccgag tagctgcaga ctccgcccgc gacgtgtgcg cgcttctctg ggccagagcg 300
agcctgtttt gtgctcgggt taagagattt gtcccagcta tacc atg ggc cgc act 356
Met Gly Arg Thr

cgg gaa gct ggc tgc gtg gcc gct ggt gtg gtt atc ggg gct ggt gcc 404
Arg Glu Ala Gly Cys Val Ala Ala Gly Val Val Ile Gly Ala Gly Ala
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tgc tac tgt gta tac aga ctg gct tgg gga aga gac gag aac gag aaa 452
Cys Tyr Cys Val Tyr Arg Leu Ala Trp Gly Arg Asp Glu Asn Glu Lys
5 10 15
atc tgg gac gaa gac gag gag tct acg gac acc tca kag att ggg gtt 500
Ile Trp Asp Glu Asp Glu Glu Ser Thr Asp Thr Ser Xaa Ile Gly Val
20 25 30
gag act gtg aaa gga gct aaa act aac gct ggg gca ggg tct ggg gcc 548
Glu Thr Val Lys Gly Ala Lys Thr Asn Ala Gly Ala Gly Ser Gly Ala
35 40 45
aaa ctt cag ggt gat tca gag gtc aag cct gag gtg agt ttg gga ctc 596
Lys Leu Gln Gly Asp Ser Glu Val Lys Pro Glu Val Ser Leu Gly Leu
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gag gat tgt ccg ggt gta aaa gag aag gcc cat tca gga tcc cac agc 644
Glu Asp Cys Pro Gly Val Lys Glu Lys Ala His Ser Gly Ser His Ser
70 75 80
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Gly Gly Gly Leu Glu Ala Lys Ala Lys Ala Leu Phe Asn Thr Leu Lys
85 90 95
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Glu Gln Ala Ser Ala Lys Ala Gly Lys Gly Ala Arg Val Gly Thr Ile
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tct ggg aac agg acc ctt gca ccg agt tta ccc tgc cca gga ggc agg 788
Ser Gly Asn Arg Thr Leu Ala Pro Ser Leu Pro Cys Pro Gly Gly Arg
115 120 125
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Gly Gly Gly Cys His Pro Thr Arg Ser Gly Ser Arg Ala Gly Gly Arg
130 135 140 145
gca agt gga aaa tcc aag gga aag gcc cga agt aag agc acc agg gct 884
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cca gct aca aca tgg cct gtc ccg aga ggc aag ttc aac ttt cct tat 932
Pro Ala Thr Thr Trp Pro Val Arg Arg Gly Lys Phe Asn Phe Pro Tyr
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Lys Ile Asp Asp Ile Leu Ser Ala Pro Asp Leu Gln Lys Val Leu Asn
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Ile Leu Glu Arg Thr Asn Asp Pro Phe Ile Gln Glu Val Ala Leu Val
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Thr Leu Gly Asn Asn Ala Ala Tyr Ser Phe Asn Gln Asn Ala Ile Arg
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		-25				-20					-15					
tgc	ggc	cag	gcg	tgg	ggt	gcg	tcg	gtg	ggc	ggc	cgc	agc	tgc	gag	gag	97
Cys	Gly	Gln	Ala	Trp	Gly	Ala	Ser	Val	Gly	Gly	Arg	Ser	Cys	Glu	Glu	
		-10				-5							1			
ctc	act	gcg	gtc	cta	acc	ccg	ccg	cag	ctc	ctc	gga	cgc	agg	ttt	aac	145
Leu	Thr	Ala	Val	Leu	Thr	Pro	Pro	Gln	Leu	Leu	Gly	Arg	Arg	Phe	Asn	
	5					10					15					
ttc	ttt	att	caa	caa	aaa	tgc	gga	ttc	aga	aaa	gca	ccc	agg	aag	gtt	193
Phe	Phe	Ile	Gln	Gln	Lys	Cys	Gly	Phe	Arg	Lys	Ala	Pro	Arg	Lys	Val	
20					25					30					35	
gaa	cct	cga	aga	tca	gac	cca	ggg	aca	agt	ggt	gaa	gca	tac	aag	aga	241
Glu	Pro	Arg	Arg	Ser	Asp	Pro	Gly	Thr	Ser	Gly	Glu	Ala	Tyr	Lys	Arg	
				40					45					50		
agt	gct	ttg	att	cct	cct	gtg	gaa	gaa	aca	gtc	ttt	tat	cct	tct	ccc	289
Ser	Ala	Leu	Ile	Pro	Pro	Val	Glu	Glu	Thr	Val	Phe	Tyr	Pro	Ser	Pro	
			55					60					65			
tat	cct	ata	agg	agt	ctc	ata	aaa	cct	tta	ttt	ttt	act	ggt	ggg	ttt	337
Tyr	Pro	Ile	Arg	Ser	Leu	Ile	Lys	Pro	Leu	Phe	Phe	Thr	Val	Gly	Phe	
		70				75						80				
aca	ggc	tgt	gca	ttt	gga	tca	gct	gct	att	tgg	caa	tat	gaa	tca	ctg	385
Thr	Gly	Cys	Ala	Phe	Gly	Ser	Ala	Ala	Ile	Trp	Gln	Tyr	Glu	Ser	Leu	
	85					90					95					
aaa	tcc	agg	gtc	cag	agt	tat	ttt	gat	ggg	ata	aaa	gct	gat	tgg	ttg	433
Lys	Ser	Arg	Val	Gln	Ser	Tyr	Phe	Asp	Gly	Ile	Lys	Ala	Asp	Trp	Leu	
	100				105				110						115	
gat	agc	ata	aga	cca	caa	aaa	gaa	gga	gac	ttc	aga	aag	gag	att	aac	481
Asp	Ser	Ile	Arg	Pro	Gln	Lys	Glu	Gly	Asp	Phe	Arg	Lys	Glu	Ile	Asn	
				120					125				130			
aag	tgg	tgg	aat	aac	cta	agt	gat	ggc	cag	cgg	act	gtg	aca	ggt	att	529
Lys	Trp	Trp	Asn	Asn	Leu	Ser	Asp	Gly	Gln	Arg	Thr	Val	Thr	Gly	Ile	
			135					140				145				
ata	gct	gca	aat	gtc	ctt	gta	ttc	tgt	tta	tgg	aga	gta	cct	tct	ctg	577
Ile	Ala	Ala	Asn	Val	Leu	Val	Phe	Cys	Leu	Trp	Arg	Val	Pro	Ser	Leu	
		150					155					160				
cag	cgg	aca	atg	atc	aga	tat	ttc	aca	tcg	aat	cca	gcc	tca	aag	gtc	625
Gln	Arg	Thr	Met	Ile	Arg	Tyr	Phe	Thr	Ser	Asn	Pro	Ala	Ser	Lys	Val	
		165				170					175					
ctt	tgt	tct	cca	atg	ttg	ctg	tca	aca	ttc	agt	cat	ttc	tcc	tta	ttt	673
Leu	Cys	Ser	Pro	Met	Leu	Leu	Ser	Thr	Phe	Ser	His	Phe	Ser	Leu	Phe	
	180				185					190					195	
cac	atg	gca	gca	aat	atg	tat	gtt	ttg	tgg	agc	ttc	tct	tcc	agc	ata	721
His	Met	Ala	Ala	Asn	Met	Tyr	Val	Leu	Trp	Ser	Phe	Ser	Ser	Ser	Ile	
			200						205				210			
gtg	aac	att	ctg	ggt	caa	gag	cag	ttc	atg	gca	gtg	tac	cta	tct	gca	769
Val	Asn	Ile	Leu	Gly	Gln	Glu	Gln	Phe	Met	Ala	Val	Tyr	Leu	Ser	Ala	
			215					220				225				
ggt	gtt	att	tcc	aat	ttt	gtc	agt	tac	gtg	ggt	aaa	gtt	gcc	aca	gga	817
Gly	Val	Ile	Ser	Asn	Phe	Val	Ser	Tyr	Val	Gly	Lys	Val	Ala	Thr	Gly	
		230					235					240				
aga	tat	gga	cca	tca	ctt	ggt	gca	gcc	ctg	aaa	gcc	att	atc	gcc	atg	865
Arg	Tyr	Gly	Pro	Ser	Leu	Gly	Ala	Ala	Leu	Lys	Ala	Ile	Ile	Ala	Met	
		245				250					255					
gat	aca	gca	gga	atg	atc	ctg	gga	tgg	aaa	ttt	ttt	gat	cat	gcg	gca	913
Asp	Thr	Ala	Gly	Met	Ile	Leu	Gly	Trp	Lys	Phe	Phe	Asp	His	Ala	Ala	

260	cat ctt ggg gga gct ctt ttt gga ata tgg tat gtt act tac ggt cat	265	Leu Gly Gly Ala Leu Phe Gly Ile Trp Tyr Val Thr Tyr Gly His	270	961
	His Leu Gly Gly Ala Leu Phe Gly Ile Trp Tyr Val Thr Tyr Gly His				
	gaa ctg att tgg aag aac agg gag ccg cta gtg aaa atc tgg cat gaa	280	285	290	1009
	Glu Leu Ile Trp Lys Asn Arg Glu Pro Leu Val Lys Ile Trp His Glu				
	ata agg act aat ggc ccc aaa aaa gga ggt ggc tct aag taaaactggg	295	300	305	1058
	Ile Arg Thr Asn Gly Pro Lys Lys Gly Gly Gly Ser Lys				
	attggacagt agtgggtgcat ctgggtccttg ccgcctgaga gcccaggag acatcgggcta	310	315	320	1118
	gagtgacat ggctatgctc ccgtctggaa gatgccagca tctggcctcc cacttttttc				1178
	agctgtgtcc cccagtcctg gtcttttttag aatgtgaatg atgataaagt tgtgaaataa				1238
	aggtttctat ctagtttgca aaaaaaaaaa aaaaa				1273

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 <213> Homo sapiens

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Leu Thr Pro Pro Gln Leu Leu Gly Arg Arg Phe Asn Phe Phe Ile Gln	10	15	20
Gln Lys Cys Gly Phe Arg Lys Ala Pro Arg Lys Val Glu Pro Arg Arg	25	30	35
Ser Asp Pro Gly Thr Ser Gly Glu Ala Tyr Lys Arg Ser Ala Leu Ile	40	45	50
Pro Pro Val Glu Glu Thr Val Phe Tyr Pro Ser Pro Tyr Pro Ile Arg	55	60	65
Ser Leu Ile Lys Pro Leu Phe Phe Thr Val Gly Phe Thr Gly Cys Ala	75	80	85
Phe Gly Ser Ala Ala Ile Trp Gln Tyr Glu Ser Leu Lys Ser Arg Val	90	95	100
Gln Ser Tyr Phe Asp Gly Ile Lys Ala Asp Trp Leu Asp Ser Ile Arg	105	110	115
Pro Gln Lys Glu Gly Asp Phe Arg Lys Glu Ile Asn Lys Trp Trp Asn	120	125	130
Asn Leu Ser Asp Gly Gln Arg Thr Val Thr Gly Ile Ile Ala Ala Asn	135	140	145
Val Leu Val Phe Cys Leu Trp Arg Val Pro Ser Leu Gln Arg Thr Met	155	160	165
Ile Arg Tyr Phe Thr Ser Asn Pro Ala Ser Lys Val Leu Cys Ser Pro	170	175	180
Met Leu Leu Ser Thr Phe Ser His Phe Ser Leu Phe His Met Ala Ala	185	190	195
Asn Met Tyr Val Leu Trp Ser Phe Ser Ser Ser Ile Val Asn Ile Leu	200	205	210
Gly Gln Glu Gln Phe Met Ala Val Tyr Leu Ser Ala Gly Val Ile Ser	215	220	225
Asn Phe Val Ser Tyr Val Gly Lys Val Ala Thr Gly Arg Tyr Gly Pro	235	240	245
Ser Leu Gly Ala Ala Leu Lys Ala Ile Ile Ala Met Asp Thr Ala Gly	250	255	260
Met Ile Leu Gly Trp Lys Phe Phe Asp His Ala Ala His Leu Gly Gly	265	270	275

Ala Leu Phe Gly Ile Trp Tyr Val Thr Tyr Gly His Glu Leu Ile Trp  
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 Gly Pro Lys Lys Gly Gly Ser Lys  
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<220>  
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 Met Asp Ser Ser Thr Ala His Ser Pro Val Phe Leu Val  
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 Phe Pro Pro Glu Ile Thr Ala Ser Glu Tyr Glu Ser Thr Glu Leu Ser  
 15 20 25  
 gcc acg acc ttt tca act caa agc ccc ttg caa aaa tta ttt gct aga 207  
 Ala Thr Thr Phe Ser Thr Gln Ser Pro Leu Gln Lys Leu Phe Ala Arg  
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 aaa atg aaa atc tta ggg act atc cag atc ctg ttt gga att atg acc 255  
 Lys Met Lys Ile Leu Gly Thr Ile Gln Ile Leu Phe Gly Ile Met Thr  
 50 55 60  
 ttt tct ttt gga gtt atc ttc ctt ttc acc ttg tta aaa cca tat cca 303  
 Phe Ser Phe Gly Val Ile Phe Leu Phe Thr Leu Leu Lys Pro Tyr Pro  
 65 70 75  
 agg ttt ccc ttt ata ttt ctt tca gga tat cca ttc tgg ggc tct gtt 351  
 Arg Phe Pro Phe Ile Phe Leu Ser Gly Tyr Pro Phe Trp Gly Ser Val  
 80 85 90  
 ttg ttc att aat tct gga gcc ttc cta att gca gtg aaa aga aaa acc 399  
 Leu Phe Ile Asn Ser Gly Ala Phe Leu Ile Ala Val Lys Arg Lys Thr  
 95 100 105  
 aca gaa act ctg ata ata ttg agc cga ata atg aat ttt ctt agt gcc 447  
 Thr Glu Thr Leu Ile Ile Leu Ser Arg Ile Met Asn Phe Leu Ser Ala  
 110 115 120 125  
 ctg gga gca ata gct gga atc att ctc ctc aca ttt ggt ttc atc cta 495  
 Leu Gly Ala Ile Ala Gly Ile Ile Leu Leu Thr Phe Gly Phe Ile Leu  
 130 135 140  
 gat caa aac tac att tgt ggt tat tct cac caa aat agt cag tgt aag 543  
 Asp Gln Asn Tyr Ile Cys Gly Tyr Ser His Gln Asn Ser Gln Cys Lys

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gct gtt act gtc ctg ttc ttg gga att ttg att aca ttg atg act ttc 591
Ala Val Thr Val Leu Phe Leu Gly Ile Leu Ile Thr Leu Met Thr Phe
      160      165      170
agc att att gaa tta ttc att tct ctg cct ttc tca att ttg ggg tgc 639
Ser Ile Ile Glu Leu Phe Ile Ser Leu Pro Phe Ser Ile Leu Gly Cys
      175      180      185
cac tca gag gat tgt gat tgt gaa caa tgt tgt tgactagcac tgtgagaata 692
His Ser Glu Asp Cys Asp Cys Glu Gln Cys Cys
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      35      40      45
Ile Leu Gly Thr Ile Gln Ile Leu Phe Gly Ile Met Thr Phe Ser Phe
50      55      60
Gly Val Ile Phe Leu Phe Thr Leu Leu Lys Pro Tyr Pro Arg Phe Pro
65      70      75      80
Phe Ile Phe Leu Ser Gly Tyr Pro Phe Trp Gly Ser Val Leu Phe Ile
      85      90      95
Asn Ser Gly Ala Phe Leu Ile Ala Val Lys Arg Lys Thr Thr Glu Thr
100      105      110
Leu Ile Ile Leu Ser Arg Ile Met Asn Phe Leu Ser Ala Leu Gly Ala
115      120      125
Ile Ala Gly Ile Ile Leu Leu Thr Phe Gly Phe Ile Leu Asp Gln Asn
130      135      140
Tyr Ile Cys Gly Tyr Ser His Gln Asn Ser Gln Cys Lys Ala Val Thr
145      150      155      160
Val Leu Phe Leu Gly Ile Leu Ile Thr Leu Met Thr Phe Ser Ile Ile
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Glu Leu Phe Ile Ser Leu Pro Phe Ser Ile Leu Gly Cys His Ser Glu
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atg ggc atg agt agc ttg aaa ctg ctg aag tat gtc ctg ttt ttc ttc 166  
Met Gly Met Ser Ser Leu Lys Leu Leu Lys Tyr Val Leu Phe Phe Phe  
1 5 10 15  
aac ttg ctc ttt tgg atc tgt ggc tgc tgc att ttg ggc ttt ggg atc 214  
Asn Leu Leu Phe Trp Ile Cys Gly Cys Cys Ile Leu Gly Phe Gly Ile  
20 25 30  
tac ctg ctg atc cac aac aac ttc gga gtg ctc ttc cat aac ctc ccc 262  
Tyr Leu Leu Ile His Asn Asn Phe Gly Val Leu Phe His Asn Leu Pro  
35 40 45  
tcc ctc acg ctg ggc aat gtg ttt gtc atc gtg ggc tct att atc atg 310  
Ser Leu Thr Leu Gly Asn Val Phe Val Ile Val Gly Ser Ile Ile Met  
50 55 60  
gta gtt gcc ttc ctg ggc tgc atg ggc tct atc aag gaa aac aag tgt 358  
Val Val Ala Phe Leu Gly Cys Met Gly Ser Ile Lys Glu Asn Lys Cys  
65 70 75 80  
ctg ctt atg tgc ttc ttc atc ctg ctg ctg att atc ctc ctt gct gag 406  
Leu Leu Met Ser Phe Phe Ile Leu Leu Leu Ile Ile Leu Leu Ala Glu  
85 90 95  
gtg acc ttg gcc atc ctg ctc ttt gtg gct aag ggt ctg acc gac agc 454  
Val Thr Leu Ala Ile Leu Leu Phe Val Ala Lys Gly Leu Thr Asp Ser  
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Ile His Arg Tyr His Ser Asp Asn Ser Thr Lys Ala Ala Trp Asp Ser  
115 120 125  
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Ile Gln Ser Phe Leu Gln Cys Cys Gly Ile Asn Gly Thr Ser Asp Trp  
130 135 140  
acc agt ggc cca cca gca tct tgc ccc tca gat cga aaa gtg gag ggt 598  
Thr Ser Gly Pro Pro Ala Ser Cys Pro Ser Asp Arg Lys Val Glu Gly  
145 150 155 160  
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Cys Tyr Ala Lys Ala Arg Leu Trp Phe His Ser Asn Phe Phe Ile Arg  
165 170 175  
ggg cct tat tgatgtgttc taagtctttc cagaaaaaaa ctatccagtg 695  
Gly Pro Tyr  
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<213> Homo sapiens

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Asn Leu Leu Phe Trp Ile Cys Gly Cys Cys Ile Leu Gly Phe Gly Ile  
20 25 30  
Tyr Leu Leu Ile His Asn Asn Phe Gly Val Leu Phe His Asn Leu Pro  
35 40 45  
Ser Leu Thr Leu Gly Asn Val Phe Val Ile Val Gly Ser Ile Ile Met  
50 55 60



Val Val Ala Phe Leu Gly Cys Met Gly Ser Ile Lys Glu Asn Lys Cys  
65 70 75 80  
Leu Leu Met Ser Phe Phe Ile Leu Leu Leu Ile Ile Leu Leu Ala Glu  
85 90 95  
Val Thr Leu Ala Ile Leu Leu Phe Val Ala Lys Gly Leu Thr Asp Ser  
100 105 110  
Ile His Arg Tyr His Ser Asp Asn Ser Thr Lys Ala Ala Trp Asp Ser  
115 120 125  
Ile Gln Ser Phe Leu Gln Cys Cys Gly Ile Asn Gly Thr Ser Asp Trp  
130 135 140  
Thr Ser Gly Pro Pro Ala Ser Cys Pro Ser Asp Arg Lys Val Glu Gly  
145 150 155 160  
Cys Tyr Ala Lys Ala Arg Leu Trp Phe His Ser Asn Phe Phe Ile Arg  
165 170 175  
Gly Pro Tyr

<210> 37  
<211> 517  
<212> DNA  
<213> Homo sapiens

<220>  
<221> 5'UTR  
<222> 1..16

<220>  
<221> CDS  
<222> 17..259

<220>  
<221> 3'UTR  
<222> 260..517

<400> 37  
ttccatagaa tgggag atg tca cca ggg cag cct atg aca ttc ccc cca gag 52  
Met Ser Pro Gly Gln Pro Met Thr Phe Pro Pro Glu  
1 5 10  
gcc ctg tgg gtg acc gtg ggg ctg tct gtc tgt ctc att gca ctg ctg 100  
Ala Leu Trp Val Thr Val Gly Leu Ser Val Cys Leu Ile Ala Leu Leu  
15 20 25  
gtg gcc ctg gct ttc gtg tgc tgg aga aag atc aaa cag agc tgt gag 148  
Val Ala Leu Ala Phe Val Cys Trp Arg Lys Ile Lys Gln Ser Cys Glu  
30 35 40  
gag gag aat gca gga gct gag gac cag gat ggg gag gga gaa ggc tcc 196  
Glu Glu Asn Ala Gly Ala Glu Asp Gln Asp Gly Glu Gly Glu Gly Ser  
45 50 55 60  
aag aca gcc ctg cag cct ctg aaa cac tct gac agc aaa gaa gat gat 244  
Lys Thr Ala Leu Gln Pro Leu Lys His Ser Asp Ser Lys Glu Asp Asp  
65 70 75  
gga caa gaa ata gcc tgaccatgag gaccagggag ctgctacccc tccctacagc 299  
Gly Gln Glu Ile Ala  
80  
tcctaccctc tggctgcaat ggggctgcac tgtgagccct gcccccaaca gatgcaccc 359  
gctctgacag gtgggctcct tctccaaagg atgcgataca cagaccactg tgcagcctta 419  
tttctccaat ggacatgatt cccaagtcac cctgctgcct tttttcttat agacacaatg 479  
aacagaccac ccacaacctt agttctctaa gtcaccc 517

<210> 38  
<211> 81  
<212> PRT  
<213> Homo sapiens

<400> 38

Met Ser Pro Gly Gln Pro Met Thr Phe Pro Pro Glu Ala Leu Trp Val  
 1 5 10 15  
 Thr Val Gly Leu Ser Val Cys Leu Ile Ala Leu Leu Val Ala Leu Ala  
 20 25 30  
 Phe Val Cys Trp Arg Lys Ile Lys Gln Ser Cys Glu Glu Glu Asn Ala  
 35 40 45  
 Gly Ala Glu Asp Gln Asp Gly Glu Gly Glu Gly Ser Lys Thr Ala Leu  
 50 55 60  
 Gln Pro Leu Lys His Ser Asp Ser Lys Glu Asp Asp Gly Gln Glu Ile  
 65 70 75 80  
 Ala

<210> 39  
 <211> 1816  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> 5'UTR  
 <222> 1..259

<220>  
 <221> CDS  
 <222> 260..1048

<220>  
 <221> 3'UTR  
 <222> 1049..1816

<220>  
 <221> polyA\_signal  
 <222> 1782..1787

<220>  
 <221> polyA\_site  
 <222> 1801..1816

<400> 39  
 actctggggc cattgccagc cggctgtagg cattcagggc agtgtcttct gcattctocta 60  
 ggaacctcgg gagcggcagc tccggcgccct ggtagcagaga ggcgggttcc ggagatcccg 120  
 gcctcacttc gtcccactgt ggtagggggg gagtcctgcg aatgttaagt gatttgctca 180  
 aggtgcccat ttcgcaggaa ttggagccca ggccagttct ctgagcctat cattagggct 240  
 aaaggagtgc gtgatcaga atg gtg tct gga cgg ttc tac ttg tcc tgc ctg 292  
 Met Val Ser Gly Arg Phe Tyr Leu Ser Cys Leu  
 -15 -10  
 ctg ctg ggg tcc ctg ggc tct atg tgc atc ctc ttc act atc tac tgg 340  
 Leu Leu Gly Ser Leu Gly Ser Met Cys Ile Leu Phe Thr Ile Tyr Trp  
 -5 1 5  
 atg cag tac tgg cgt ggt ggc ttt gcc tgg aat ggc agc atc tac atg 388  
 Met Gln Tyr Trp Arg Gly Gly Phe Ala Trp Asn Gly Ser Ile Tyr Met  
 10 15 20  
 ttc aac tgg cac cca gtg ctt atg gtt gct ggc atg gtg gta ttc tat 436  
 Phe Asn Trp His Pro Val Leu Met Val Ala Gly Met Val Val Phe Tyr  
 25 30 35 40  
 gga ggt gcg tca ctg gtg tac cgc ctg ccc cag tcg tgg gtg ggg ccc 484  
 Gly Gly Ala Ser Leu Val Tyr Arg Leu Pro Gln Ser Trp Val Gly Pro  
 45 50 55  
 aaa ctg ccc tgg aaa ctc ctc cat gca gcg ctg cac ctg atg gcc ttc 532  
 Lys Leu Pro Trp Lys Leu Leu His Ala Ala Leu His Leu Met Ala Phe  
 60 65 70  
 gtc ctc act gtt gtg ggg ctg gtt gct gtc ttt acg ttt cac aac cat 580  
 Val Leu Thr Val Val Gly Leu Val Ala Val Phe Thr Phe His Asn His  
 75 80 85





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Ala Asp Gln Asn Cys Thr Gln Glu Cys Val Ser Asp Ser Glu Cys Ala
      15      20      25
gac aac ctc aag tgc tgc agc gcg ggc tgt gcc acc ttc tgc tct ctg 306
Asp Asn Leu Lys Cys Cys Ser Ala Gly Cys Ala Thr Phe Cys Ser Leu
      30      35      40
ccc aat gat aag gag ggt tcc tgc ccc cag gtg aac att aac ttt ccc 354
Pro Asn Asp Lys Glu Gly Ser Cys Pro Gln Val Asn Ile Asn Phe Pro
      45      50      55
cag ctc ggc ctc tgt cgg gac cag tgc cag gtg gac agc cag tgt cct 402
Gln Leu Gly Leu Cys Arg Asp Gln Cys Gln Val Asp Ser Gln Cys Pro
      60      65      70      75
ggc cag atg aaa tgc tgc cgc aat ggc tgt ggg aag gtg tcc tgt gtc 450
Gly Gln Met Lys Cys Cys Arg Asn Gly Cys Gly Lys Val Ser Cys Val
      80      85      90
act ccc aat ttc tgagctccag ccaccaccag gctgagcagt gaggagagaa 502
Thr Pro Asn Phe
      95
agtttctgcc tggccctgca tctgggttcca gccacactgc cctcccccttt ttcggggactc 562
tgtattccct cttgggctga ccacagcttc tccctttccc aaccaataaa gtaaccactt 622
tcagcaaaaa aaaaaaaaaa a 643

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<210> 42
<211> 124
<212> PRT
<213> Homo sapiens

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<220>
<221> SIGNAL
<222> 1..30

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<400> 42
Met Pro Ala Cys Arg Leu Gly Pro Leu Ala Ala Ala Leu Leu Leu Ser
-30      -25      -20      -15
Leu Leu Leu Phe Gly Phe Thr Leu Val Ser Gly Thr Gly Ala Glu Lys
      -10      -5      1
Thr Gly Val Cys Pro Glu Leu Gln Ala Asp Gln Asn Cys Thr Gln Glu
      5      10      15
Cys Val Ser Asp Ser Glu Cys Ala Asp Asn Leu Lys Cys Cys Ser Ala
      20      25      30
Gly Cys Ala Thr Phe Cys Ser Leu Pro Asn Asp Lys Glu Gly Ser Cys
      35      40      45      50
Pro Gln Val Asn Ile Asn Phe Pro Gln Leu Gly Leu Cys Arg Asp Gln
      55      60      65
Cys Gln Val Asp Ser Gln Cys Pro Gly Gln Met Lys Cys Cys Arg Asn
      70      75      80
Gly Cys Gly Lys Val Ser Cys Val Thr Pro Asn Phe
      85      90

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<210> 43
<211> 501
<212> DNA
<213> Homo sapiens

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<220>
<221> 5'UTR
<222> 1..227

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<220>
<221> CDS
<222> 228..501

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<400> 43
actcttactc tttctctctc actctctctc ttttcccacc cttaagccaa gtacagggat 60

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agttgtctca tcattggtgg cttaaaatga tgtttttgaa caagaagaca ccccatggga 120
ctgatctcaa atgcagctgt gactaaaacc tctaggtgct gtgctgtcct gaggcctggg 180
ccatggtgcc caaggaaagc ccctgaagct caccaggagg aagaagc atg cag ggc 236
                                Met Gln Gly
                                -30
act cct gga ggc ggg acg cgc cct ggg cca tcc ccc gtg gac agg cgg 284
Thr Pro Gly Gly Gly Thr Arg Pro Gly Pro Ser Pro Val Asp Arg Arg
                                -25                                -20                                -15
aca ctc ctg gtc ttc agc ttt atc ctg gca gca gct ttg ggc caa atg 332
Thr Leu Leu Val Phe Ser Phe Ile Leu Ala Ala Ala Leu Gly Gln Met
                                -10                                -5                                1
aat ttc aca ggg gac cag gtt ctt cga gtc ctg gcc aaa gat gag aag 380
Asn Phe Thr Gly Asp Gln Val Leu Arg Val Leu Ala Lys Asp Glu Lys
                                5                                10                                15
cag ctt tca ctt ctc ggg gat ctg gag ggc ctg aaa ccc cag aag gtg 428
Gln Leu Ser Leu Leu Gly Asp Leu Glu Gly Leu Lys Pro Gln Lys Val
20                                25                                30                                35
gac ttc tgg cgt ggc cca gcc agg ccc agc ctc cct gtg gat atg aga 476
Asp Phe Trp Arg Gly Pro Ala Arg Pro Ser Leu Pro Val Asp Met Arg
                                40                                45                                50
gtt cct ttc tcc gaa ctg aaa gac a 501
Val Pro Phe Ser Glu Leu Lys Asp
                                55

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<210> 44  
 <211> 91  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> 1..33

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<400> 44
Met Gln Gly Thr Pro Gly Gly Gly Thr Arg Pro Gly Pro Ser Pro Val
                                -30                                -25                                -20
Asp Arg Arg Thr Leu Leu Val Phe Ser Phe Ile Leu Ala Ala Ala Leu
                                -15                                -10                                -5
Gly Gln Met Asn Phe Thr Gly Asp Gln Val Leu Arg Val Leu Ala Lys
1                                5                                10                                15
Asp Glu Lys Gln Leu Ser Leu Leu Gly Asp Leu Glu Gly Leu Lys Pro
                                20                                25                                30
Gln Lys Val Asp Phe Trp Arg Gly Pro Ala Arg Pro Ser Leu Pro Val
                                35                                40                                45
Asp Met Arg Val Pro Phe Ser Glu Leu Lys Asp
                                50                                55

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<210> 45  
 <211> 960  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> 5'UTR  
 <222> 1..97

<220>  
 <221> CDS  
 <222> 98..934

<220>  
 <221> 3'UTR  
 <222> 935..960

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<400> 45
ataatcacct ctcattccag actatgtttag gtcttaatgg tgggaggacg cccgagtgct 60
cggcccgttt caccgagagg aggaaggaca ctggggtc atg acg cca tca gaa ggc 115
                                Met Thr Pro Ser Glu Gly
                                1       5
gcc aga gca ggg acc gga cgc gag ttg gag atg ttg gac tcg ctg ttg 163
Ala Arg Ala Gly Thr Gly Arg Glu Leu Glu Met Leu Asp Ser Leu Leu
                                10      15      20
gcc ttg ggc ggc ctg gtg ctg ctt cgg gat tcc gtg gag tgg gag ggg 211
Ala Leu Gly Gly Leu Val Leu Leu Arg Asp Ser Val Glu Trp Glu Gly
                                25      30      35
cgc agt ctc ttg aag ggc ctt gtc aag aaa tct gca ctg tgt ggg gag 259
Arg Ser Leu Leu Lys Ala Leu Val Lys Lys Ser Ala Leu Cys Gly Glu
                                40      45      50
caa gtg cat atc ctg ggc tgt gaa gtg agc gag gaa gag ttt cgt gaa 307
Gln Val His Ile Leu Gly Cys Glu Val Ser Glu Glu Glu Phe Arg Glu
55                                60      65      70
ggg ttt gac tct gat atc aac aat cgg ctg gtt tac cat gac ttc ttc 355
Gly Phe Asp Ser Asp Ile Asn Asn Arg Leu Val Tyr His Asp Phe Phe
                                75      80      85
aga gac cct ctc aac tgg tca aaa act gag gag gcc ttt cct ggg ggg 403
Arg Asp Pro Leu Asn Trp Ser Lys Thr Glu Glu Ala Phe Pro Gly Gly
                                90      95      100
ccg ctg gga gcc ttg aga gcc atg tgc aag agg aca gat cct gtt cct 451
Pro Leu Gly Ala Leu Arg Ala Met Cys Lys Arg Thr Asp Pro Val Pro
                                105     110     115
gtc acc att gct ctc gat tca ctc agc tgg ctg cta ctt cgc ctt ccc 499
Val Thr Ile Ala Leu Asp Ser Leu Ser Trp Leu Leu Leu Arg Leu Pro
120                                125     130
tgc acc aca ctc tgc cag gtc ctg cat gct gtg agc cat cag gac tct 547
Cys Thr Thr Leu Cys Gln Val Leu His Ala Val Ser His Gln Asp Ser
135                                140     145     150
tgt cct ggt gac agc tcc tca gtg ggg aaa gtg agt gtg ctg ggc ttg 595
Cys Pro Gly Asp Ser Ser Ser Val Gly Lys Val Ser Val Leu Gly Leu
                                155     160     165
cta cat gaa gag ctt cat gga cca ggc cct gtg gga gct ctc agc agc 643
Leu His Glu Glu Leu His Gly Pro Gly Pro Val Gly Ala Leu Ser Ser
170                                175     180
ctt gct cag act gag gtg acc ctg ggc ggt acc atg ggc cag gcc tcg 691
Leu Ala Gln Thr Glu Val Thr Leu Gly Gly Thr Met Gly Gln Ala Ser
185                                190     195
gcc cac atc ctg tgt cgg agg ccc cga cag cgc cca act gac cag act 739
Ala His Ile Leu Cys Arg Arg Pro Arg Gln Arg Pro Thr Asp Gln Thr
200                                205     210
cag tgg ttc tcc atc ctt ccg gac ttc agc ctg gat ctc caa gag ggg 787
Gln Trp Phe Ser Ile Leu Pro Asp Phe Ser Leu Asp Leu Gln Glu Gly
215                                220     225     230
ccc tct gta gag tcc cag ccc tac tcc gat cct cat ata ccc ccg gta 835
Pro Ser Val Glu Ser Gln Pro Tyr Ser Asp Pro His Ile Pro Pro Val
                                235     240     245
tct aag aat gcc aag gcc aga aca agg aaa tgt agt tta gta tct ggt 883
Ser Lys Asn Ala Lys Ala Arg Thr Arg Lys Cys Ser Leu Val Ser Gly
250                                255     260
cac ggg aga gaa aat aaa agc tgc aga ggt tgg ggg tgg ggt cag gga 931
His Gly Arg Glu Asn Lys Ser Cys Arg Gly Trp Gly Trp Gly Gln Gly
265                                270     275
ttc tagggatggg gcagagtggc agcatc 960
Phe

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<210> 46  
 <211> 279  
 <212> PRT

<213> Homo sapiens

<400> 46

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Met Thr Pro Ser Glu Gly Ala Arg Ala Gly Thr Gly Arg Glu Leu Glu
1      5      10      15
Met Leu Asp Ser Leu Leu Ala Leu Gly Gly Leu Val Leu Leu Arg Asp
20     25     30
Ser Val Glu Trp Glu Gly Arg Ser Leu Leu Lys Ala Leu Val Lys Lys
35     40     45
Ser Ala Leu Cys Gly Glu Gln Val His Ile Leu Gly Cys Glu Val Ser
50     55     60
Glu Glu Glu Phe Arg Glu Gly Phe Asp Ser Asp Ile Asn Asn Arg Leu
65     70     75     80
Val Tyr His Asp Phe Arg Asp Pro Leu Asn Trp Ser Lys Thr Glu
85     90     95
Glu Ala Phe Pro Gly Gly Pro Leu Gly Ala Leu Arg Ala Met Cys Lys
100    105    110
Arg Thr Asp Pro Val Pro Val Thr Ile Ala Leu Asp Ser Leu Ser Trp
115    120    125
Leu Leu Leu Arg Leu Pro Cys Thr Thr Leu Cys Gln Val Leu His Ala
130    135    140
Val Ser His Gln Asp Ser Cys Pro Gly Asp Ser Ser Ser Val Gly Lys
145    150    155    160
Val Ser Val Leu Gly Leu Leu His Glu Glu Leu His Gly Pro Gly Pro
165    170    175
Val Gly Ala Leu Ser Ser Leu Ala Gln Thr Glu Val Thr Leu Gly Gly
180    185    190
Thr Met Gly Gln Ala Ser Ala His Ile Leu Cys Arg Arg Pro Arg Gln
195    200    205
Arg Pro Thr Asp Gln Thr Gln Trp Phe Ser Ile Leu Pro Asp Phe Ser
210    215    220
Leu Asp Leu Gln Glu Gly Pro Ser Val Glu Ser Gln Pro Tyr Ser Asp
225    230    235    240
Pro His Ile Pro Pro Val Ser Lys Asn Ala Lys Ala Arg Thr Arg Lys
245    250    255
Cys Ser Leu Val Ser Gly His Gly Arg Glu Asn Lys Ser Cys Arg Gly
260    265    270
Trp Gly Trp Gly Gln Gly Phe
275

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<210> 47

<211> 1294

<212> DNA

<213> Homo sapiens

<220>

<221> 5'UTR

<222> 1..266

<220>

<221> CDS

<222> 267..1139

<220>

<221> 3'UTR

<222> 1140..1294

<220>

<221> polyA\_signal

<222> 1246..1251

<220>

<221> polyA\_site



<222> 1279..1294

<400> 47

gactctgagg ctccctcttt gctctaacag acagcagcga ctttaggctg gataatagtc 60  
aaattcttac ctgcgtcttt cactgctagt aagatcagat tgcgtttctt tcagttactc 120  
ttcaatcgcc agtttcttga tctgcttcta aaagaagaag tagagaagat aaatcctgtc 180  
ttcaatacct ggaaggaaaa acaaaataac ctcaactccg ttttgaaaaa aacattccaa 240  
gaactttcat cagagatttt acttag atg att tac aca atg aag aaa gta cat 293  
Met Ile Tyr Thr Met Lys Lys Val His  
-25 -20  
gca ctt tgg gct tct gta tgc ctg ctg ctt aat ctt gcc cct gcc cct 341  
Ala Leu Trp Ala Ser Val Cys Leu Leu Leu Asn Leu Ala Pro Ala Pro  
-15 -10 -5  
ctt aat gct gat tct gag gaa gat gaa gaa cac aca att atc aca gat 389  
Leu Asn Ala Asp Ser Glu Glu Asp Glu Glu His Thr Ile Ile Thr Asp  
1 5 10  
acg gag ttg cca cca ctg aaa ctt atg cat tca ttt tgt gca ttc aag 437  
Thr Glu Leu Pro Pro Leu Lys Leu Met His Ser Phe Cys Ala Phe Lys  
15 20 25 30  
gcg gat gat ggc cca tgt aaa gca atc atg aaa aga ttt ttc ttc aat 485  
Ala Asp Asp Gly Pro Cys Lys Ala Ile Met Lys Arg Phe Phe Phe Asn  
35 40 45  
att ttc act cga cag tgc gaa gaa ttt ata tat ggg gga tgt gaa gga 533  
Ile Phe Thr Arg Gln Cys Glu Glu Phe Ile Tyr Gly Gly Cys Glu Gly  
50 55 60  
aat cag aat cga ttt gaa agt ctg gaa gag tgc aaa aaa atg tgt aca 581  
Asn Gln Asn Arg Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr  
65 70 75  
aga gaa aag cca gat ttc tgc ttt ttg gaa gaa gat cct gga ata tgt 629  
Arg Glu Lys Pro Asp Phe Cys Phe Leu Glu Glu Asp Pro Gly Ile Cys  
80 85 90  
cga ggt tat att acc agg tat ttt tat aac aat cag aca aaa cag tgt 677  
Arg Gly Tyr Ile Thr Arg Tyr Phe Tyr Asn Asn Gln Thr Lys Gln Cys  
95 100 105 110  
gaa cgt ttc aag tat ggt gga tgc ctg ggc aat atg aac aat ttt gag 725  
Glu Arg Phe Lys Tyr Gly Gly Cys Leu Gly Asn Met Asn Asn Phe Glu  
115 120 125  
aca ctg gaa gaa tgc aag aac att tgt gaa gat ggt ccg aat ggt ttc 773  
Thr Leu Glu Glu Cys Lys Asn Ile Cys Glu Asp Gly Pro Asn Gly Phe  
130 135 140  
cag gtg gat aat tat gga acc cag ctc aat gct gtg aat aac tcc ctg 821  
Gln Val Asp Asn Tyr Gly Thr Gln Leu Asn Ala Val Asn Asn Ser Leu  
145 150 155  
act ccg caa tca acc aag gtt ccc agc ctt ttt gaa ttt cac ggt ccc 869  
Thr Pro Gln Ser Thr Lys Val Pro Ser Leu Phe Glu Phe His Gly Pro  
160 165 170  
tca tgg tgt ctc act cca gca gac aga gga ttg tgt cgt gcc aat gag 917  
Ser Trp Cys Leu Thr Pro Ala Asp Arg Gly Leu Cys Arg Ala Asn Glu  
175 180 185 190  
aac aga ttc tac tac aat tca gtc att ggg aaa tgc cgc cca ttt aag 965  
Asn Arg Phe Tyr Tyr Asn Ser Val Ile Gly Lys Cys Arg Pro Phe Lys  
195 200 205  
tac agt gga tgt ggg gga aat gaa aac aat ttt act tcc aaa caa gaa 1013  
Tyr Ser Gly Cys Gly Gly Asn Glu Asn Asn Phe Thr Ser Lys Gln Glu  
210 215 220  
tgt ctg agg gca tgt aaa aaa ggt ttc atc caa aga ata tca aaa gga 1061  
Cys Leu Arg Ala Cys Lys Lys Gly Phe Ile Gln Arg Ile Ser Lys Gly  
225 230 235  
ggc cta att aaa acc aaa aga aaa aga aag aag cag aga gtg aaa ata 1109  
Gly Leu Ile Lys Thr Lys Arg Lys Arg Lys Lys Gln Arg Val Lys Ile  
240 245 250  
gca tat gaa gaa att ttt gtt aaa aat atg tgaatttggt atagcaatgt 1159  
Ala Tyr Glu Glu Ile Phe Val Lys Asn Met

[illegible]

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<220>
<221> SIGNAL
<222> 1..28
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<210> 49
<211> 1194
<212> DNA
<213> Homo sapiens
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<221> CDS  
<222> 48..1100

<220>  
<221> 3'UTR  
<222> 1101..1194

<220>  
<221> polyA\_signal  
<222> 1159..1164

<220>  
<221> polyA\_site  
<222> 1179..1194

<400> 49  
ctcctcagct tcaggcacca ccactgacct gggacagtga atcgaca atg ccg tct 56  
Met Pro Ser  
tct gtc tcg tgg ggc atc ctc ctg ctg gca ggc ctg tgc tgc ctg gtc 104  
Ser Val Ser Trp Gly Ile Leu Leu Leu Ala Gly Leu Cys Cys Leu Val  
-20 -15 -10 -5  
cct gtc tcc ctg ggg acc aag gct gac act cac gat gaa atc ctg gag 152  
Pro Val Ser Leu Gly Thr Lys Ala Asp Thr His Asp Glu Ile Leu Glu  
1 5 10  
ggc ctg aat ttc aac ctc acg gag att ccg gag gct cag atc cat gaa 200  
Gly Leu Asn Phe Asn Leu Thr Glu Ile Pro Glu Ala Gln Ile His Glu  
15 20 25  
ggc ttc cag gaa ctc ctc cgt acc ctc aac cag cca gac agc cag ctc 248  
Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn Gln Pro Asp Ser Gln Leu  
30 35 40  
cag ctg acc acc ggc aat ggc ctg ttc ctc agc gag ggc ctg aag cta 296  
Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu Ser Glu Gly Leu Lys Leu  
45 50 55 60  
gtg gat aag ttt ttg gag gat gtt aaa aag ttg tac cac tca gaa gcc 344  
Val Asp Lys Phe Leu Glu Asp Val Lys Lys Leu Tyr His Ser Glu Ala  
65 70 75  
ttc act gtc aac ttc ggg gac acc gaa gag gcc aag aaa cag atc aac 392  
Phe Thr Val Asn Phe Gly Asp Thr Glu Glu Ala Lys Lys Gln Ile Asn  
80 85 90  
gat tac gtg gag aag ggt act caa ggg aaa att gtg gat ttg gtc aag 440  
Asp Tyr Val Glu Lys Gly Thr Gln Gly Lys Ile Val Asp Leu Val Lys  
95 100 105  
gag ctt gac aga gac aca gtt ttt gct ctg gtg aat tac atc ttc ttt 488  
Glu Leu Asp Arg Asp Thr Val Phe Ala Leu Val Asn Tyr Ile Phe Phe  
110 115 120  
aaa ggc aaa tgg gag aga ccc ttt gaa gtc aag gac acc gag gaa gag 536  
Lys Gly Lys Trp Glu Arg Pro Phe Glu Val Lys Asp Thr Glu Glu Glu  
125 130 135 140  
gac ttc cac gtg gac cag gtg acc acc gtg aag gtg cct atg atg aag 584  
Asp Phe His Val Asp Gln Val Thr Thr Val Lys Val Pro Met Met Lys  
145 150 155  
cgt tta ggc atg ttt aac atc cag cac tgt aag aag ctg tcc agc tgg 632  
Arg Leu Gly Met Phe Asn Ile Gln His Cys Lys Lys Leu Ser Ser Trp  
160 165 170  
gtg ctg ctg atg aaa tac ctg ggc aat gcc acc gcc atc ttc ttc ctg 680  
Val Leu Leu Met Lys Tyr Leu Gly Asn Ala Thr Ala Ile Phe Phe Leu  
175 180 185  
cct gat gag ggg aaa cta cag cac ctg gaa aat gaa ctc acc cac gat 728  
Pro Asp Glu Gly Lys Leu Gln His Leu Glu Asn Glu Leu Thr His Asp  
190 195 200  
atc atc acc aag ttc ctg gaa aat gaa gac aga agg tct gcc agc tta 776  
Ile Ile Thr Lys Phe Leu Glu Asn Glu Asp Arg Arg Ser Ala Ser Leu  
205 210 215 220





				45					50					55				
tat	ggg	gga	tgt	gaa	gga	aat	cag	aat	cga	ttt	gaa	agt	ctg	gaa	gag			586
Tyr	Gly	Gly	Cys	Glu	Gly	Asn	Gln	Asn	Arg	Phe	Glu	Ser	Leu	Glu	Glu			
			60						65					70				
tgc	aaa	aaa	atg	tgt	aca	aga	gaa	aag	cca	gat	ttc	tgc	ttt	ttg	gaa			634
Cys	Lys	Lys	Met	Cys	Thr	Arg	Glu	Lys	Pro	Asp	Phe	Cys	Phe	Leu	Glu			
			75						80					85				
gaa	gat	cct	gga	ata	tgt	cga	ggg	tat	att	acc	agg	tat	ttt	tat	aac			682
Glu	Asp	Pro	Gly	Ile	Cys	Arg	Gly	Tyr	Ile	Thr	Arg	Tyr	Phe	Tyr	Asn			
			90						95					100				
aat	cag	aca	aaa	cag	tgt	gaa	cgt	ttc	aag	tat	ggg	gga	tgc	ctg	ggc			730
Asn	Gln	Thr	Lys	Gln	Cys	Glu	Arg	Phe	Lys	Tyr	Gly	Gly	Cys	Leu	Gly			
					110									120				
aat	atg	aac	aat	ttt	gag	aca	ctg	gaa	gaa	tgc	aag	aac	att	tgt	gaa			778
Asn	Met	Asn	Asn	Phe	Glu	Thr	Leu	Glu	Glu	Cys	Lys	Asn	Ile	Cys	Glu			
					125									135				
gat	ggg	ccg	aat	ggg	ttc	cag	gtg	gat	aat	tat	gga	acc	cag	ctc	aat			826
Asp	Gly	Pro	Asn	Gly	Phe	Gln	Val	Asp	Asn	Tyr	Gly	Thr	Gln	Leu	Asn			
			140											150				
gct	gtg	aat	aac	tcc	ctg	act	ccg	caa	tca	acc	aag	gtt	ccc	agc	ctt			874
Ala	Val	Asn	Asn	Ser	Leu	Thr	Pro	Gln	Ser	Thr	Lys	Val	Pro	Ser	Leu			
			155											165				
ttt	gaa	ttt	cac	ggg	ccc	tca	tgg	tgt	ctc	act	cca	gca	gac	aga	gga			922
Phe	Glu	Phe	His	Gly	Pro	Ser	Trp	Cys	Leu	Thr	Pro	Ala	Asp	Arg	Gly			
			170											180				
ttg	tgt	cgt	gcc	aat	gag	aac	aga	ttc	tac	tac	aat	tca	gtc	att	ggg			970
Leu	Cys	Arg	Ala	Asn	Glu	Asn	Arg	Phe	Tyr	Tyr	Asn	Ser	Val	Ile	Gly			
					190									200				
aaa	tgc	cgc	cca	ttt	aag	tac	agt	gga	tgt	ggg	gga	aat	gaa	aac	aat			1018
Lys	Cys	Arg	Pro	Phe	Lys	Tyr	Ser	Gly	Cys	Gly	Gly	Asn	Glu	Asn	Asn			
					205									215				
ttt	act	tcc	aaa	caa	gaa	tgt	ctg	agg	gca	tgt	aaa	aaa	ggg	ttc	atc			1066
Phe	Thr	Ser	Lys	Gln	Glu	Cys	Leu	Arg	Ala	Cys	Lys	Lys	Gly	Phe	Ile			
					220									230				
caa	aga	ata	tca	aaa	gga	ggc	cta	att	aaa	acc	aaa	aga	aaa	aga	aag			1114
Gln	Arg	Ile	Ser	Lys	Gly	Gly	Leu	Ile	Lys	Thr	Lys	Arg	Lys	Arg	Lys			
					235									245				
aag	cag	aga	gtg	aaa	ata	gca	tat	gaa	gaa	att	ttt	gtt	aaa	aat	atg			1162
Lys	Gln	Arg	Val	Lys	Ile	Ala	Tyr	Glu	Glu	Ile	Phe	Val	Lys	Asn	Met			
					250									260				
tgaatttggt	atagcaatgt	aacattaatt	ctactaaata	ttttatatga	aatgtttcac													1222
tatgattttc	tattttttctt	ctaaaatgct	tttaattaat	atgttcatta	aatttttctat													1282
gcttattgta	cttgttatca	aaaaaaaaaa	aaaaaa															1317

<210> 52  
 <211> 291  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> 1..28

<400> 52  
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 -25 -20 -15  
 Leu Leu Leu Asn Leu Ala Pro Ala Pro Leu Asn Ala Asp Ser Glu Glu  
 -10 -5 1  
 Asp Glu Glu His Thr Ile Ile Thr Asp Thr Glu Leu Pro Pro Leu Lys  
 5 10 15 20  
 Leu Met His Ser Phe Cys Ala Phe Lys Ser Asp Asp Gly Pro Cys Lys  
 25 30 35  
 Ala Ile Met Lys Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu









45	50	55	
ggg aag tac tac aag gag gca acg ctc acc atg gac cag gtc agc tcc			244
Gly Lys Tyr Tyr Lys Glu Ala Thr Leu Thr Met Asp Gln Val Ser Ser			
60	65	70	
ctg cca gct ctg cgg gtc aac cct ttc aga gac cgt atc tgc aga gtg			292
Leu Pro Ala Leu Arg Val Asn Pro Phe Arg Asp Arg Ile Cys Arg Val			
75	80	85	
ttc tcc cac aaa ggc atg ttc tcc ttt gag gat gtg ctg ggc atg gca			340
Phe Ser His Lys Gly Met Phe Ser Phe Glu Asp Val Leu Gly Met Ala			
90	95	100	105
tct gtg ttc agc gag cag gcc tgc cca agc ctg aag att gag tat gcc			388
Ser Val Phe Ser Glu Gln Ala Cys Pro Ser Leu Lys Ile Glu Tyr Ala			
110	115	120	
ttt cgc atc tat gat ttt aat gag aat ggc ttc att gat gag gag gat			436
Phe Arg Ile Tyr Asp Phe Asn Glu Asn Gly Phe Ile Asp Glu Glu Asp			
125	130	135	
ctg cag agg atc atc ctg cga ctg ctg aac agt gat gac atg tct gag			484
Leu Gln Arg Ile Ile Leu Arg Leu Leu Asn Ser Asp Asp Met Ser Glu			
140	145	150	
gac ctc ctg atg gac ctc acg aac cac gtc ctg agt gag tgc gat ctg			532
Asp Leu Leu Met Asp Leu Thr Asn His Val Leu Ser Glu Ser Asp Leu			
155	160	165	
gac aat gac aac atg ctg tcc ttc tca gag ttt gaa cat gca atg gcc			580
Asp Asn Asp Asn Met Leu Ser Phe Ser Glu Phe Glu His Ala Met Ala			
170	175	180	185
aag tct cca gat ttc atg aac tcc ttt cgg att cac ttc tgg gga tgc			628
Lys Ser Pro Asp Phe Met Asn Ser Phe Arg Ile His Phe Trp Gly Cys			
190	195	200	
tgatgtagcg gcaaatacct gacatggcag cctcgaggga gaccacagga atcgaacccc			688
ctccagcact ggagggagct gggtttgaagt atgactttgt actgggcccc cactcacctc			748
tagaatattg tttattagat aaaagaaaaa gcttttcctt agcccgaataa aaaaaaaaaa			808
t			809

<210> 56  
 <211> 201  
 <212> PRT  
 <213> Homo sapiens

<400> 56

Met Leu Glu Val Ser Asp Ala Leu Gly Gly Pro Gly Arg Val Pro Gly	
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Ala Thr Ala Gly Met Asn Gly Val Asp Thr Ser Leu Leu Cys Asp Leu	
20 25 30	
Leu Gln Ala Leu Thr Phe Leu Thr Arg Asn Glu Ile Leu Cys Ile His	
35 40 45	
Asp Thr Phe Leu Lys Leu Cys Pro Pro Gly Lys Tyr Tyr Lys Glu Ala	
50 55 60	
Thr Leu Thr Met Asp Gln Val Ser Ser Leu Pro Ala Leu Arg Val Asn	
65 70 75 80	
Pro Phe Arg Asp Arg Ile Cys Arg Val Phe Ser His Lys Gly Met Phe	
85 90 95	
Ser Phe Glu Asp Val Leu Gly Met Ala Ser Val Phe Ser Glu Gln Ala	
100 105 110	
Cys Pro Ser Leu Lys Ile Glu Tyr Ala Phe Arg Ile Tyr Asp Phe Asn	
115 120 125	
Glu Asn Gly Phe Ile Asp Glu Glu Asp Leu Gln Arg Ile Ile Leu Arg	
130 135 140	
Leu Leu Asn Ser Asp Asp Met Ser Glu Asp Leu Leu Met Asp Leu Thr	
145 150 155 160	
Asn His Val Leu Ser Glu Ser Asp Leu Asp Asn Asp Asn Met Leu Ser	
165 170 175	
Phe Ser Glu Phe Glu His Ala Met Ala Lys Ser Pro Asp Phe Met Asn	
180 185 190	

Ser Phe Arg Ile His Phe Trp Gly Cys  
 195 200

<210> 57  
 <211> 1133  
 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> 1..475

<220>  
 <221> CDS  
 <222> 476..964

<220>  
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 <222> 965..1133

<220>  
 <221> polyA\_signal  
 <222> 1101..1106

<220>  
 <221> polyA\_site  
 <222> 1118..1133

<400> 57  
 gacataatca gagctatgct ggaggagaag agggcagcca tttgctggct ggcttgcaagt 60  
 gagccaggag gtggcaggac gagttaggag gctgggtcag tagctcgggc aagagcaggg 120  
 cccccccagg tctgaaggcc tcccaggccc ccaggccca gcgggtccca gaggagagcg 180  
 aggaccccaa ggtaactccg gtgagaaggc cgaccaggga tttcaaggcc agccaggctt 240  
 tccggggccca ccgggtccccc ctggattccc aggcaaagt ggatcacctg gcccacctgg 300  
 ccctcaagca gagaagggca gcgaagggat tcgaggccca tcaggcctgc ctggctcccc 360  
 tggggccaccg ggacctcctg ggattcaggc ccccgccggg ctggatgggt tggatgggaa 420  
 ggatggcaag cctggcttga ggggggaccc tggctctgct ggccccctg gactc atg 478  
 Met  
 1  
 gga cca ccg ggc ttt aag ggg aaa aca gga cat cct ggc ctc cca gga 526  
 Gly Pro Pro Gly Phe Lys Gly Lys Thr Gly His Pro Gly Leu Pro Gly  
 5 10 15  
 cct aag ggt gac tgt ggc aaa cca ggt cct cct ggc agc act ggc cgg 574  
 Pro Lys Gly Asp Cys Gly Lys Pro Gly Pro Pro Gly Ser Thr Gly Arg  
 20 25 30  
 cct ggc gca gag ggt gaa cct ggt gcc atg gga ccc cag gga aga ccc 622  
 Pro Gly Ala Glu Gly Glu Pro Gly Ala Met Gly Pro Gln Gly Arg Pro  
 35 40 45  
 ggt ccc ccg gga cac gtt ggg cca cca ggg cct cca ggc cag cca gga 670  
 Gly Pro Pro Gly His Val Gly Pro Pro Gly Pro Pro Gly Gln Pro Gly  
 50 55 60 65  
 cca gct ggg atc tct gca gtg ggt ctg aaa gga gac cga gga gcc acc 718  
 Pro Ala Gly Ile Ser Ala Val Gly Leu Lys Gly Asp Arg Gly Ala Thr  
 70 75 80  
 gga gaa agg ggc ctt gca ggc ctc cca ggc cag ccc ggc ccc cca ggt 766  
 Gly Glu Arg Gly Leu Ala Gly Leu Pro Gly Gln Pro Gly Pro Pro Gly  
 85 90 95  
 cct caa ggt cct cca ggc tat ggc aag atg ggt gca aca gga cca atg 814  
 Pro Gln Gly Pro Pro Gly Tyr Gly Lys Met Gly Ala Thr Gly Pro Met  
 100 105 110  
 ggc cag caa ggc atc cct ggc atc cct ggg ccc ccg ggt ccc atg ggc 862  
 Gly Gln Gln Gly Ile Pro Gly Ile Pro Gly Pro Gly Pro Met Gly  
 115 120 125





Thr Glu Glu Pro Gly Glu Ser Phe Cys Asp Lys Val Met Arg Trp Phe  
 100 105 110  
 Gln Ala Met Leu Gln Arg Leu Gln Thr Trp Trp His Gly Val Leu Ala  
 115 120 125  
 Trp Val Lys Glu Lys Val Val Ala Leu Val His Ala Val Gln Ala Leu  
 130 135 140  
 Trp Lys Gln Phe Gln Ser Phe Cys Cys Ser Leu Ser Glu Leu Phe Met  
 145 150 155 160  
 Ser Ser Phe Gln Ser Tyr Gly Ala Pro Arg Gly Asp Lys Glu Glu Leu  
 165 170 175  
 Thr Pro Gln Lys Cys Ser Glu Pro Gln Ser Ser Lys  
 180 185

<210> 61  
 <211> 862  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> 5'UTR  
 <222> 1..158

<220>  
 <221> CDS  
 <222> 159..764

<220>  
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 <222> 765..862

<400> 61  
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 tggctgctgc cttaagacgt gcagcctggg ccgtggctgt cactgcgttc ggaccagac 120  
 ccgctgcagg cagcagcagc ccccgcccgcc gcagcagc atg gag ctc tgg ggg gcc 176  
 Met Glu Leu Trp Gly Ala  
 -20 -15  
 tac ctc ctc ctc tgc ctc ttc tcc ctc ctg acc cag gtc acc acc gag 224  
 Tyr Leu Leu Leu Cys Leu Phe Ser Leu Leu Thr Gln Val Thr Thr Glu  
 -10 -5 1  
 cca cca acc cag aag ccc aag aag att gta aat gcc aag aaa gat gtt 272  
 Pro Pro Thr Gln Lys Pro Lys Lys Ile Val Asn Ala Lys Lys Asp Val  
 5 10 15  
 gtg aac aca aag atg ttt gag gag ctc aag agc cgt ctg gac acc ctg 320  
 Val Asn Thr Lys Met Phe Glu Glu Leu Lys Ser Arg Leu Asp Thr Leu  
 20 25 30  
 gcc cag gag gtg gcc ctg ctg aag gag cag cag gcc ctg cag acg gtc 368  
 Ala Gln Glu Val Ala Leu Leu Lys Glu Gln Gln Ala Leu Gln Thr Val  
 35 40 45 50  
 tgc ctg aag ggg acc aag gtg cac atg aaa tgc ttt ctg gcc ttc acc 416  
 Cys Leu Lys Gly Thr Lys Val His Met Lys Cys Phe Leu Ala Phe Thr  
 55 60 65  
 cag acg aag acc ttc cac gag tcc agc gag gac tgc atc tcg cgc ggg 464  
 Gln Thr Lys Thr Phe His Glu Ser Ser Glu Asp Cys Ile Ser Arg Gly  
 70 75 80  
 ggc acc ctg agc acc cct cag act ggc tcg gag aac gac gcc ctg tat 512  
 Gly Thr Leu Ser Thr Pro Gln Thr Gly Ser Glu Asn Asp Ala Leu Tyr  
 85 90 95  
 gag tac ctg cgc cag agc gtg ggc aac gag gcc gag atc tgg ctg ggc 560  
 Glu Tyr Leu Arg Gln Ser Val Gly Asn Glu Ala Glu Ile Trp Leu Gly  
 100 105 110  
 ctc aac gac atg gcg gcc gag ggc acc tgg gtg gac atg acc ggc gcc 608  
 Leu Asn Asp Met Ala Ala Glu Gly Thr Trp Val Asp Met Thr Gly Ala  
 115 120 125 130

cgc atc gcc tac aag aac tgg gag act gag atc acc gcg caa ccc gat 656  
 Arg Ile Ala Tyr Lys Asn Trp Glu Thr Glu Ile Thr Ala Gln Pro Asp  
 135 140 145  
 ggc ggc aag acc gag aac tgc gcg gtc ctg tca ggc gcg gcc aac ggc 704  
 Gly Gly Lys Thr Glu Asn Cys Ala Val Leu Ser Gly Ala Ala Asn Gly  
 150 155 160  
 aag tgg ttc gac aag cgc tgc cgc gat cag ctg ccc tac atc tgc cag 752  
 Lys Trp Phe Asp Lys Arg Cys Arg Asp Gln Leu Pro Tyr Ile Cys Gln  
 165 170 175  
 ttc ggc atc gtg tagccggcgg ggcggggggcc gtggggggggc tggaggaggg 804  
 Phe Gly Ile Val  
 180  
 caggagccgc gggaggccgg gaggagggtg gggaccttgc agcccccatc ctctccgt 862

<210> 62  
 <211> 202  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> 1..21

<400> 62  
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 Thr Gln Val Thr Thr Glu Pro Pro Thr Gln Lys Pro Lys Lys Ile Val  
 -5 1 5 10  
 Asn Ala Lys Lys Asp Val Val Asn Thr Lys Met Phe Glu Glu Leu Lys  
 15 20 25  
 Ser Arg Leu Asp Thr Leu Ala Gln Glu Val Ala Leu Leu Lys Glu Gln  
 30 35 40  
 Gln Ala Leu Gln Thr Val Cys Leu Lys Gly Thr Lys Val His Met Lys  
 45 50 55  
 Cys Phe Leu Ala Phe Thr Gln Thr Lys Thr Phe His Glu Ser Ser Glu  
 60 65 70 75  
 Asp Cys Ile Ser Arg Gly Gly Thr Leu Ser Thr Pro Gln Thr Gly Ser  
 80 85 90  
 Glu Asn Asp Ala Leu Tyr Glu Tyr Leu Arg Gln Ser Val Gly Asn Glu  
 95 100 105  
 Ala Glu Ile Trp Leu Gly Leu Asn Asp Met Ala Ala Glu Gly Thr Trp  
 110 115 120  
 Val Asp Met Thr Gly Ala Arg Ile Ala Tyr Lys Asn Trp Glu Thr Glu  
 125 130 135  
 Ile Thr Ala Gln Pro Asp Gly Gly Lys Thr Glu Asn Cys Ala Val Leu  
 140 145 150 155  
 Ser Gly Ala Ala Asn Gly Lys Trp Phe Asp Lys Arg Cys Arg Asp Gln  
 160 165 170  
 Leu Pro Tyr Ile Cys Gln Phe Gly Ile Val  
 175 180

<210> 63  
 <211> 618  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> 5'UTR  
 <222> 1..194

<220>  
 <221> CDS  
 <222> 195..587

<220>  
 <221> 3'UTR  
 <222> 588..618

<220>  
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 <222> 578..583

<220>  
 <221> polyA\_site  
 <222> 604..618

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 cctacaaggg cctccctgac acccaagttc atattgctca gaaacagtga acttgagttt 120  
 ttcgttttac cttgatctct ctctgacaaa gaaatccaga tgatgcgaga cctgatgaag 180  
 acaatacatg gaaa atg aca gtc ttg gaa ata act ttg gct gtc atc ctg 230  
 Met Thr Val Leu Glu Ile Thr Leu Ala Val Ile Leu  
 -20 -15 -10  
 act cta ctg gga ctt gcc atc ctg gct att ttg tta aca aga tgg gca 278  
 Thr Leu Leu Gly Leu Ala Ile Leu Ala Ile Leu Leu Thr Arg Trp Ala  
 -5 1 5  
 cga cgt aag caa agt gaa atg cat atc tcc aga tac agt tca gaa caa 326  
 Arg Arg Lys Gln Ser Glu Met His Ile Ser Arg Tyr Ser Ser Glu Gln  
 10 15 20  
 agt gct aga ctt ctg gac tat gag gat ggt aga gga tcc cga cat gca 374  
 Ser Ala Arg Leu Leu Asp Tyr Glu Asp Gly Arg Gly Ser Arg His Ala  
 25 30 35  
 tat tca aca caa agt gag aga tcc aaa aga gat tac aca cca tca acc 422  
 Tyr Ser Thr Gln Ser Glu Arg Ser Lys Arg Asp Tyr Thr Pro Ser Thr  
 40 45 50 55  
 aac tct cta gca ctg tct cga tca agt att gct tta cct caa gga tcc 470  
 Asn Ser Leu Ala Leu Ser Arg Ser Ser Ile Ala Leu Pro Gln Gly Ser  
 60 65 70  
 atg agt agt ata aaa tgt tta caa aca act gaa gaa ctt cct tcc aga 518  
 Met Ser Ser Ile Lys Cys Leu Gln Thr Thr Glu Glu Leu Pro Ser Arg  
 75 80 85  
 act gca gga gcc atg agt aag ttc ttt ttc tgc cct tta att ctc atg 566  
 Thr Ala Gly Ala Met Ser Lys Phe Phe Phe Cys Pro Leu Ile Leu Met  
 90 95 100  
 tgc ttt gct tta cta aac tgt tagaatatgt aagacgaaaa aaaaaaaaaa a 618  
 Cys Phe Ala Leu Leu Asn Cys  
 105 110

<210> 64  
 <211> 131  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> 1..22

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 Ser Glu Met His Ile Ser Arg Tyr Ser Ser Glu Gln Ser Ala Arg Leu  
 15 20 25  
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 30 35 40







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 <222> 63..572

<220>  
 <221> 3'UTR  
 <222> 573..789

<220>  
 <221> polyA\_signal  
 <222> 750..755

<220>  
 <221> polyA\_site  
 <222> 774..789

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 ga atg cgg ctt caa ggg gct atc ttt gtg ctc ctg ccc cac ctg ggg 107  
 Met Arg Leu Gln Gly Ala Ile Phe Val Leu Leu Pro His Leu Gly  
 1 5 10 15  
 ccc atc ctg gtc tgg ctg ttc act cgt gat cac atg tct ggt tgg tgt 155  
 Pro Ile Leu Val Trp Leu Phe Thr Arg Asp His Met Ser Gly Trp Cys  
 20 25 30  
 gag ggc ccg agg atg ctg tcc tgg tgc cca ttc tac aaa gtc tta ttg 203  
 Glu Gly Pro Arg Met Leu Ser Trp Cys Pro Phe Tyr Lys Val Leu Leu  
 35 40 45  
 ctt gta cag aca gcc atc tac tct gtc gtg ggc tat gcc tcc tac ctg 251  
 Leu Val Gln Thr Ala Ile Tyr Ser Val Val Gly Tyr Ala Ser Tyr Leu  
 50 55 60  
 gtg tgg aag gac ctg gga ggg ggc ttg ggg tgg ccc ctg gcc ctg cct 299  
 Val Trp Lys Asp Leu Gly Gly Leu Gly Trp Pro Leu Ala Leu Pro  
 65 70 75  
 ctt cgc ctc tat gct gtt cag ctc acc atc agc tgg act gtc ctg gtt 347  
 Leu Arg Leu Tyr Ala Val Gln Leu Thr Ile Ser Trp Thr Val Leu Val  
 80 85 90 95  
 ctc ttt ttc aca gtc cac aac cct ggt ctg gcc ctg ctg cac ctg ctg 395  
 Leu Phe Phe Thr Val His Asn Pro Gly Leu Ala Leu Leu His Leu Leu  
 100 105 110  
 ctg ctg tat ggg ctg gtg gtg agc aca gca ctg atc tgg cat ccc atc 443  
 Leu Leu Tyr Gly Leu Val Val Ser Thr Ala Leu Ile Trp His Pro Ile  
 115 120 125  
 aac aaa ctg gct gcc ctg tta ctg ctg ccc tac cta gcc tgg ctc acc 491  
 Asn Lys Leu Ala Ala Leu Leu Leu Leu Pro Tyr Leu Ala Trp Leu Thr  
 130 135 140  
 gtg act tca gcc ctc acc tac cac ctg tgg agg gac agc ctt tgt cca 539  
 Val Thr Ser Ala Leu Thr Tyr His Leu Trp Arg Asp Ser Leu Cys Pro  
 145 150 155  
 gtg cac cag cct cag ccc acg gag aag agt gac tgaggcccta gggcatggga 592  
 Val His Gln Pro Gln Pro Thr Glu Lys Ser Asp  
 160 165 170  
 gaggagggac gcccagggtg gggaggaaga gtctgcaagc agggctgtgg agttaggggtt 652  
 caccccaatg ggaccaccct cctgggtccc ctggtgccgt ttttccttag aaatcagaga 712  
 aatgggaaag ggggggaaac tgattttaca cttaaataat aaaatcctat tagtaactcc 772  
 gaaaaaaaa aaaaaaa 789

<210> 68  
 <211> 170  
 <212> PRT  
 <213> Homo sapiens

<400> 68

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Ile Leu Val Trp Leu Phe Thr Arg Asp His Met Ser Gly Trp Cys Glu
20      25      30
Gly Pro Arg Met Leu Ser Trp Cys Pro Phe Tyr Lys Val Leu Leu Leu
35      40      45
Val Gln Thr Ala Ile Tyr Ser Val Val Gly Tyr Ala Ser Tyr Leu Val
50      55      60
Trp Lys Asp Leu Gly Gly Gly Leu Gly Trp Pro Leu Ala Leu Pro Leu
65      70      75      80
Arg Leu Tyr Ala Val Gln Leu Thr Ile Ser Trp Thr Val Leu Val Leu
85      90      95
Phe Phe Thr Val His Asn Pro Gly Leu Ala Leu Leu His Leu Leu Leu
100     105     110
Leu Tyr Gly Leu Val Val Ser Thr Ala Leu Ile Trp His Pro Ile Asn
115     120     125
Lys Leu Ala Ala Leu Leu Leu Leu Pro Tyr Leu Ala Trp Leu Thr Val
130     135     140
Thr Ser Ala Leu Thr Tyr His Leu Trp Arg Asp Ser Leu Cys Pro Val
145     150     155     160
His Gln Pro Gln Pro Thr Glu Lys Ser Asp
165     170

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 <212> DNA  
 <213> Homo sapiens

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 <222> 1..66  
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 <222> 67..2427

<220>  
 <221> 3'UTR  
 <222> 2428..2556

<220>  
 <221> polyA\_signal  
 <222> 2522..2527

<220>  
 <221> polyA\_site  
 <222> 2541..2556

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cgccacc atg ttc cgc ctc tgg ttg ctg ctg gcc ggg ctc tgc ggc ctc 108
      Met Phe Arg Leu Trp Leu Leu Leu Ala Gly Leu Cys Gly Leu
      -15      -10      -5
ctg gcg tca aga ccc ggt ttt caa aat tca ctt cta cag atc gta att 156
Leu Ala Ser Arg Pro Gly Phe Gln Asn Ser Leu Leu Gln Ile Val Ile
1      5      10      15
cca gag aaa atc caa aca aat aca aat gac agt tca gaa ata gaa tat 204
Pro Glu Lys Ile Gln Thr Asn Thr Asn Asp Ser Ser Glu Ile Glu Tyr
20      25      30
gaa caa ata tcc tat att att cca ata gat gag aaa ctg tac act gtg 252
Glu Gln Ile Ser Tyr Ile Ile Pro Ile Asp Glu Lys Leu Tyr Thr Val
35      40      45
cac ctt aaa caa aga tat ttt tta aca gat aat ttt atg atc tat ttg 300

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Ser Ser Ser Glu Gly Ser Thr Gln Thr Tyr Ala Gly Gln Thr Arg Ser  
 720 725 730 735  
 gaa agc agc agt caa gct gat act agc aaa tcc aaa tca gaa gat agt 2364  
 Glu Ser Ser Ser Gln Ala Asp Thr Ser Lys Ser Lys Ser Glu Asp Ser  
 740 745 750  
 gct gaa gca tat act agc aga tcc aaa tca cag gac agt acc caa aca 2412  
 Ala Glu Ala Tyr Thr Ser Arg Ser Lys Ser Gln Asp Ser Thr Gln Thr  
 755 760 765  
 caa agc agt agt aac tagtgattcc ttcagaaggc aacggataac atcgagagtc 2467  
 Gln Ser Ser Ser Asn  
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 1 5 10 15  
 Lys Ile Gln Thr Asn Thr Asn Asp Ser Ser Glu Ile Glu Tyr Glu Gln  
 20 25 30  
 Ile Ser Tyr Ile Ile Pro Ile Asp Glu Lys Leu Tyr Thr Val His Leu  
 35 40 45  
 Lys Gln Arg Tyr Phe Leu Thr Asp Asn Phe Met Ile Tyr Leu Tyr Asn  
 50 55 60  
 Gln Gly Ser Met Asn Thr Tyr Ser Ser Asp Ile Gln Thr Gln Cys Tyr  
 65 70 75 80  
 Tyr Gln Gly Asn Ile Glu Glu Tyr Pro Asp Ser Met Val Thr Leu Ser  
 85 90 95  
 Thr Cys Ser Gly Leu Arg Gly Ile Leu Gln Phe Glu Asn Val Ser Tyr  
 100 105 110  
 Gly Ile Glu Pro Leu Glu Ser Ala Val Glu Phe Gln His Val Leu His  
 115 120 125  
 Lys Leu Lys Asn Glu Asp Asn Asp Ile Ala Ile Phe Ile Asp Arg Ser  
 130 135 140  
 Leu Lys Glu Gln Pro Met Asp Asp Asn Ile Phe Ile Ser Glu Lys Ser  
 145 150 155 160  
 Glu Pro Ala Val Pro Asp Leu Phe Pro Leu Tyr Leu Glu Met His Ile  
 165 170 175  
 Val Val Asp Lys Thr Leu Tyr Asp Tyr Trp Gly Ser Asp Ser Met Ile  
 180 185 190  
 Val Thr Asn Lys Val Ile Glu Ile Val Gly Leu Ala Asn Ser Met Phe  
 195 200 205  
 Thr Gln Phe Lys Val Thr Ile Val Leu Ser Ser Leu Glu Leu Trp Ser  
 210 215 220  
 Asp Glu Asn Lys Ile Ser Thr Val Gly Glu Ala Asp Glu Leu Leu Gln  
 225 230 235 240  
 Lys Phe Leu Glu Trp Lys Gln Ser Tyr Leu Asn Leu Arg Pro His Asp  
 245 250 255  
 Ile Ala Tyr Leu Leu Ile Tyr Met Asp Tyr Pro Arg Tyr Leu Gly Ala  
 260 265 270  
 Val Phe Pro Gly Thr Met Cys Ile Thr Arg Tyr Ser Ala Gly Val Ala  
 275 280 285  
 Leu Tyr Pro Lys Glu Ile Thr Leu Glu Ala Phe Ala Val Ile Val Thr

	290						295				300					
Gln 305	Met	Leu	Ala	Leu	Ser	Leu	Gly	Ile	Ser	Tyr	Asp	Asp	Pro	Lys	Lys	
Cys	Gln	Cys	Ser	Glu	Ser	Thr	Cys	Ile	Met	Asn	Pro	Glu	Val	Val	Gln	
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Ser	Asn	Gly	Val	Lys	Thr	Phe	Ser	Ser	Cys	Ser	Leu	Arg	Ser	Phe	Gln	
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Asn	Phe	Ile	Ser	Asn	Val	Gly	Val	Lys	Cys	Leu	Gln	Asn	Lys	Pro	Gln	
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Met	Gln	Lys	Lys	Ser	Pro	Lys	Pro	Val	Cys	Gly	Asn	Gly	Arg	Leu	Glu	
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Ser	Cys	Cys	Asp	Phe	Arg	Thr	Cys	Val	Leu	Lys	Asp	Gly	Ala	Lys	Cys	
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Tyr	Lys	Gly	Leu	Cys	Cys	Lys	Asp	Cys	Gln	Ile	Leu	Gln	Ser	Gly	Val	
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Glu	Cys	Arg	Pro	Lys	Ala	His	Pro	Glu	Cys	Asp	Ile	Ala	Glu	Asn	Cys	
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Asn	Gly	Ser	Ser	Pro	Glu	Cys	Gly	Pro	Asp	Ile	Thr	Leu	Ile	Asn	Gly	
	450					455				460						
Leu	Ser	Cys	Lys	Asn	Asn	Lys	Phe	Ile	Cys	Tyr	Asp	Gly	Asp	Cys	His	
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Asp	Leu	Asp	Ala	Arg	Cys	Glu	Ser	Val	Phe	Gly	Lys	Gly	Ser	Arg	Asn	
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Ala	Pro	Phe	Ala	Cys	Tyr	Glu	Glu	Ile	Gln	Ser	Gln	Ser	Asp	Arg	Phe	
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Arg	Asn	Leu	Ile	Cys	Gly	Arg	Leu	Val	Cys	Thr	Tyr	Pro	Thr	Arg	Lys	
	530				535					540						
Pro	Phe	His	Gln	Glu	Asn	Gly	Asp	Val	Ile	Tyr	Ala	Phe	Val	Arg	Asp	
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Ser	Val	Cys	Ile	Thr	Val	Asp	Tyr	Lys	Leu	Pro	Arg	Thr	Val	Pro	Asp	
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Pro	Leu	Ala	Val	Lys	Asn	Gly	Ser	Gln	Cys	Asp	Ile	Gly	Arg	Val	Cys	
			580					585					590			
Val	Asn	Arg	Glu	Cys	Val	Glu	Ser	Arg	Ile	Ile	Lys	Ala	Ser	Ala	His	
	595					600					605					
Val	Cys	Ser	Gln	Gln	Cys	Ser	Gly	His	Gly	Val	Cys	Asp	Ser	Arg	Asn	
	610				615					620						
Lys	Cys	His	Cys	Ser	Pro	Gly	Tyr	Lys	Pro	Pro	Asn	Cys	Gln	Ile	Arg	
625				630					635						640	
Ser	Lys	Gly	Phe	Ser	Ile	Phe	Pro	Glu	Glu	Asp	Met	Gly	Ser	Ile	Met	
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64



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<220>  
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 cgg tca ctc cgt gtc tgt gtg tcc ctc tgg tct gtc cac cac agg cca 97  
 Arg Ser Leu Arg Val Cys Val Ser Leu Trp Ser Val His His Arg Pro  
                   1                                  5                                  10  
 cac gag tcc ctg gcc cgg gag gag gcc ctc act gca ctt ggg aag ctc 145  
 His Glu Ser Leu Ala Arg Glu Glu Ala Leu Thr Ala Leu Gly Lys Leu  
                   15                                  20                                  25                                  30  
 ctg tac ctc tta gat ggg atg ctg gat ggg cag gtg aac agt ggt ata 193  
 Leu Tyr Leu Leu Asp Gly Met Leu Asp Gly Gln Val Asn Ser Gly Ile  
                                   35                                  40                                  45  
 gca gcc act cca gcc tct gct gca gca gcc acc ctg gat gtg gct gtt 241  
 Ala Ala Thr Pro Ala Ser Ala Ala Ala Thr Leu Asp Val Ala Val  
                                   50                                  55                                  60  
 cgg aga ggc ctg tcc cac gca gcc cag agg ctg ctg tgc gtg gcc ctg 289  
 Arg Arg Gly Leu Ser His Ala Ala Gln Arg Leu Leu Cys Val Ala Leu  
                                   65                                  70                                  75  
 gga cag ctg gac cgg cct cca gac ctc gcc cat gac ggg agg agt ctg 337  
 Gly Gln Leu Asp Arg Pro Pro Asp Leu Ala His Asp Gly Arg Ser Leu  
                                   80                                  85                                  90  
 tgg ctg aac atc agg ggc aag gag gcg gct gcc cta tcc atg ttc cat 385  
 Trp Leu Asn Ile Arg Gly Lys Glu Ala Ala Ala Leu Ser Met Phe His  
                                   95                                  100                                  105                                  110  
 gtc tcc acg cca ctg cca gtg atg acc ggt ggt ttc ctg agc tgc atc 433  
 Val Ser Thr Pro Leu Pro Val Met Thr Gly Gly Phe Leu Ser Cys Ile  
                                   115                                  120                                  125  
 ttg ggc ttg gtg ctg ccc ctg gcc tat ggc ttc cag cct gac ctg gtg 481  
 Leu Gly Leu Val Leu Pro Leu Ala Tyr Gly Phe Gln Pro Asp Leu Val  
                                   130                                  135                                  140  
 ctg gtg gcg ctg ggg cct ggc cat ggc ctg cag ggc ccc cac gst gca 529  
 Leu Val Ala Leu Gly Pro Gly His Gly Leu Gln Gly Pro His Xaa Ala  
                                   145                                  150                                  155  
 ctc ctg gct gca atg ctt cgg ggg ctg gca ggg ggc cga gtc ctg gcc 577  
 Leu Leu Ala Ala Met Leu Arg Gly Leu Ala Gly Gly Arg Val Leu Ala  
                                   160                                  165                                  170  
 ctc ctg gag gag aac tcc aca ccc cag cta gca ggg atc ctg gcc cgg 625  
 Leu Leu Glu Glu Asn Ser Thr Pro Gln Leu Ala Gly Ile Leu Ala Arg

175	180	185	190	
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Val Leu Asn Gly Glu Ala Pro Pro Ser Leu Gly Pro Ser Ser Val Ala				
	195	200	205	
tcc cca gag gac gtc cag gcc ctg atg tac ctg aga ggg cag ctg gag				721
Ser Pro Glu Asp Val Gln Ala Leu Met Tyr Leu Arg Gly Gln Leu Glu				
	210	215	220	
cct cag tgg aag atg ttg cag tgc cat cct cac ctg gtg gct				763
Pro Gln Trp Lys Met Leu Gln Cys His Pro His Leu Val Ala				
	225	230	235	
tgaaatcggc caaggtggga gcattttacac cgcagaaatg acaccgcacg ccagcgcgcc				823
gcggccgcga tccggacccc aagcccacgg ctccctcgac tctggggcac ggaaccccgc				883
ccactcccaa tccccgcgcc ccgccctctc ccacccgtgc ttccccgct ccacccctca				943
cctcacctcg cccccgcccc acccatcgcg ccccggcggc tggtattgtt cggctgggct				1003
cggtcggggcg ctgtctccct cggctctgcg ggtgtcagtt cgtccggctt cctcacagcc				1063
cctcactccc ggcggctgac agcagcagcg gcggcggcgg gcggcgcctg gcgtttcgag				1123
gctgagcggc accgggggtg gggcgcgag gagagcagc agcgggagga ggagccgtgt				1183
gccctggcac tgagcggcgg cggccatggc gtacgcctat ctcttcaagt acatcataat				1243
cggcgacaca ggtgttggtt aatcatgctt attgctacag ttacagaca agaggttcag				1303
ccagtgcag accttactat tgggtgtagag ttcggtgctc gaatgataac tattgatggg				1363
aaacagataa aacttcagat atgggatacg gcagggcaag aatcctttcg ttccatcaca				1423
aggtcgtatt acagaggtgc agcaggagct ttactagttt acgatattac acggagagat				1483
acattcaacc acttgacaac ctgggttagaa gatgcccgcc agcattccaa ttccaacatg				1543
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1 5 10 15	
Ser Leu Ala Arg Glu Glu Ala Leu Thr Ala Leu Gly Lys Leu Leu Tyr	
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Leu Leu Asp Gly Met Leu Asp Gly Gln Val Asn Ser Gly Ile Ala Ala	
35 40 45	
Thr Pro Ala Ser Ala Ala Ala Ala Thr Leu Asp Val Ala Val Arg Arg	
50 55 60	
Gly Leu Ser His Ala Ala Gln Arg Leu Leu Cys Val Ala Leu Gly Gln	
65 70 75	
Leu Asp Arg Pro Pro Asp Leu Ala His Asp Gly Arg Ser Leu Trp Leu	
80 85 90 95	
Asn Ile Arg Gly Lys Glu Ala Ala Ala Leu Ser Met Phe His Val Ser	
100 105 110	
Thr Pro Leu Pro Val Met Thr Gly Gly Phe Leu Ser Cys Ile Leu Gly	
115 120 125	
Leu Val Leu Pro Leu Ala Tyr Gly Phe Gln Pro Asp Leu Val Leu Val	
130 135 140	
Ala Leu Gly Pro Gly His Gly Leu Gln Gly Pro His Xaa Ala Leu Leu	
145 150 155	
Ala Ala Met Leu Arg Gly Leu Ala Gly Gly Arg Val Leu Ala Leu Leu	



gcctgtaatc ccagctactc gggaggctga ggcaggagaa ttgcttgaac ctgggaggtg 795  
gaggttgctg tgagtggaga tcatgccatt gcactccagc ctgagcaaca agagcaaac 855  
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<222> 1..16

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Phe Pro Ala Arg Pro Gly Arg Gly Arg Pro Tyr Met Ala Ser Arg Pro  
20 25 30  
Pro Gly Asp Leu Ala Glu Ala Gly Gly Arg Ala Leu Gln Ser Leu Gln  
35 40 45  
Leu Arg Leu Leu Thr Pro Thr Phe Glu Gly Ile Asn Gly Leu Leu Leu  
50 55 60  
Lys Gln His Leu Val Gln Asn Pro Val Arg Leu Trp Gln Leu Leu Gly  
65 70 75 80  
Gly Thr Phe Tyr Phe Asn Thr Ser Arg Leu Lys Gln Lys Asn Lys Glu  
85 90 95  
Lys Asp Lys Ser Lys Gly Lys Ala Pro Glu Glu Asp Glu Gly Ile Phe  
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Ile

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Met Met Gly Val Phe Val Val Ala Ala  
1 5  
aag cga acg ccc ttt gga gct tac gga ggc ctt ctg aaa gac ttc act 162

Lys	Arg	Thr	Pro	Phe	Gly	Ala	Tyr	Gly	Gly	Leu	Leu	Lys	Asp	Phe	Thr	
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Ala	Thr	Asp	Leu	Ser	Glu	Phe	Ala	Ala	Lys	Ala	Ala	Leu	Ser	Ala	Gly	
				30					35					40		
aaa	gtc	tca	cct	gaa	aca	gtt	gac	agt	gtg	att	atg	ggc	aat	gtc	ctg	258
Lys	Val	Ser	Pro	Glu	Thr	Val	Asp	Ser	Val	Ile	Met	Gly	Asn	Val	Leu	
			45					50					55			
cag	agt	tct	tca	gat	gct	ata	tat	ttg	gca	agg	cat	gtt	ggg	ttg	cgt	306
Gln	Ser	Ser	Ser	Asp	Ala	Ile	Tyr	Leu	Ala	Arg	His	Val	Gly	Leu	Arg	
		60				65					70					
gtg	gga	atc	cca	aag	gag	acc	cca	gct	ctc	acg	att	aat	agg	ctc	tgt	354
Val	Gly	Ile	Pro	Lys	Glu	Thr	Pro	Ala	Leu	Thr	Ile	Asn	Arg	Leu	Cys	
	75					80					85					
ggg	tct	ggg	ttt	cag	tcc	att	gtg	aat	gga	tgt	cag	gaa	att	tgt	gtt	402
Gly	Ser	Gly	Phe	Gln	Ser	Ile	Val	Asn	Gly	Cys	Gln	Glu	Ile	Cys	Val	
	90				95					100					105	
aaa	gaa	gct	gaa	gtt	gtt	tta	tgt	gga	gga	acc	gaa	agc	atg	agc	caa	450
Lys	Glu	Ala	Glu	Val	Val	Leu	Cys	Gly	Gly	Thr	Glu	Ser	Met	Ser	Gln	
			110						115					120		
gct	ccc	tac	tgt	gtc	aga	aat	gtg	cgt	ttt	gga	acc	aag	ctt	gga	tca	498
Ala	Pro	Tyr	Cys	Val	Arg	Asn	Val	Arg	Phe	Gly	Thr	Lys	Leu	Gly	Ser	
			125					130					135			
gat	atc	aag	ctg	gaa	gat	tct	tta	tgg	gta	tca	tta	aca	gat	cag	cat	546
Asp	Ile	Lys	Leu	Glu	Asp	Ser	Leu	Trp	Val	Ser	Leu	Thr	Asp	Gln	His	
		140					145					150				
gtc	cag	ctc	ccc	atg	gca	atg	act	gca	gag	aat	ctt	gct	gta	aaa	cac	594
Val	Gln	Leu	Pro	Met	Ala	Met	Thr	Ala	Glu	Asn	Leu	Ala	Val	Lys	His	
	155					160					165					
aaa	ata	agc	aga	gaa	gaa	tgt	gac	aaa	tat	gcc	ctg	cag	tca	cag	cag	642
Lys	Ile	Ser	Arg	Glu	Glu	Cys	Asp	Lys	Tyr	Ala	Leu	Gln	Ser	Gln	Gln	
	170				175					180					185	
aga	tgg	aaa	gct	gct	aat	gat	gct	ggc	tac	ttt	aat	gat	gaa	atg	gca	690
Arg	Trp	Lys	Ala	Ala	Asn	Asp	Ala	Gly	Tyr	Phe	Asn	Asp	Glu	Met	Ala	
			190						195				200			
cca	att	gaa	gtg	aag	aca	aag	aaa	gga	aaa	cag	aca	atg	cag	gta	gac	738
Pro	Ile	Glu	Val	Lys	Thr	Lys	Lys	Gly	Lys	Gln	Thr	Met	Gln	Val	Asp	
		205						210					215			
gag	cat	gct	cgg	ccc	caa	acc	acc	ctg	gaa	cag	tta	cag	aaa	ctt	cct	786
Glu	His	Ala	Arg	Pro	Gln	Thr	Thr	Leu	Glu	Gln	Leu	Gln	Lys	Leu	Pro	
		220					225					230				
cca	gta	ttc	aag	aaa	gat	gga	act	gtt	act	gca	ggg	aat	gca	tcg	ggg	834
Pro	Val	Phe	Lys	Lys	Asp	Gly	Thr	Val	Thr	Ala	Gly	Asn	Ala	Ser	Gly	
	235					240				245						
gta	gct	gat	ggg	gct	gga	gct	gtt	atc	ata	gct	agt	gaa	gat	gct	gtt	882
Val	Ala	Asp	Gly	Ala	Gly	Ala	Val	Ile	Ile	Ala	Ser	Glu	Asp	Ala	Val	
	250				255					260					265	
aag	aaa	cat	aac	ttc	aca	cca	ctg	gca	aga	att	gtg	ggc	tac	ttt	gta	930
Lys	Lys	His	Asn	Phe	Thr	Pro	Leu	Ala	Arg	Ile	Val	Gly	Tyr	Phe	Val	
			270						275					280		
tct	gga	tgt	gat	ccc	tct	atc	atg	ggg	att	ggg	cct	gtc	cct	gct	atc	978
Ser	Gly	Cys	Asp	Pro	Ser	Ile	Met	Gly	Ile	Gly	Pro	Val	Pro	Ala	Ile	
			285					290					295			
agt	ggg	gca	ctg	aag	aaa	gca	gga	ctg	agt	ctt	aag	gac	atg	gat	ttg	1026
Ser	Gly	Ala	Leu	Lys	Lys	Ala	Gly	Leu	Ser	Leu	Lys	Asp	Met	Asp	Leu	
		300					305					310				
gta	gag	gtg	aat	gaa	gct	ttt	gct	ccc	cag	tac	ttg	gct	gtt	gag	agg	1074
Val	Glu	Val	Asn	Glu	Ala	Phe	Ala	Pro	Gln	Tyr	Leu	Ala	Val	Glu	Arg	
		315				320					325					
agt	ttg	gat	ctt	gac	ata	agt	aaa	acc	aat	gtg	aat	gga	gga	gcc	att	1122
Ser	Leu	Asp	Leu	Asp	Ile	Ser	Lys	Thr	Asn	Val	Asn	Gly	Gly	Ala	Ile	
	330				335					340					345	
gct	ttg	ggg	cac	cca	ctg	gga	gga	tct	gga	tca	aga	att	act	gca	cac	1170



Time (h)	Temperature (°C)	Pressure (atm)	Flow rate (L/min)	Conversion (%)	Yield (%)	Product (g)	Product (mol)	Product (L)	Product (kg)
0	25	1.0	1.0	0	0	0	0	0	0
1	25	1.0	1.0	10	10	0.1	0.001	0.1	0.1
2	25	1.0	1.0	20	20	0.2	0.002	0.2	0.2
3	25	1.0	1.0	30	30	0.3	0.003	0.3	0.3
4	25	1.0	1.0	40	40	0.4	0.004	0.4	0.4
5	25	1.0	1.0	50	50	0.5	0.005	0.5	0.5
6	25	1.0	1.0	60	60	0.6	0.006	0.6	0.6
7	25	1.0	1.0	70	70	0.7	0.007	0.7	0.7
8	25	1.0	1.0	80	80	0.8	0.008	0.8	0.8
9	25	1.0	1.0	90	90	0.9	0.009	0.9	0.9
10	25	1.0	1.0	100	100	1.0	0.010	1.0	1.0

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<222> 1..68

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<222> 1627..1642
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71

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110								115						120					
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Thr	Asp	Ser	Glu	Asp	Lys	Ala	Leu	Met	Asn	Gly	Ser	Glu	Ser	Arg	Phe				
125								130						135					
ttc	gtg	agt	tcc	tcg	cag	ggc	ctg	tca	gag	cta	cac	att	gag	aac	ctg	590			
Phe	Val	Ser	Ser	Ser	Gln	Gly	Leu	Ser	Glu	Leu	His	Ile	Glu	Asn	Leu				
140								145						150					
aac	atg	gag	gcc	gac	ccc	ggc	cag	tac	cgg	tgc	aac	ggc	acc	agc	tcc	638			
Asn	Met	Glu	Ala	Asp	Pro	Gly	Gln	Tyr	Arg	Cys	Asn	Gly	Thr	Ser	Ser				
155								160						165		170			
aag	ggc	tcc	gac	cag	gcc	atc	atc	acg	ctc	cgc	gtg	cgc	agc	cac	ctg	686			
Lys	Gly	Ser	Asp	Gln	Ala	Ile	Ile	Thr	Leu	Arg	Val	Arg	Ser	His	Leu				
175								180						185					
gcc	gcc	ctc	tgg	ccc	ttc	ctg	ggc	atc	gtg	gct	gag	gtg	ctg	gtg	ctg	734			
Ala	Ala	Leu	Trp	Pro	Phe	Leu	Gly	Ile	Val	Ala	Glu	Val	Leu	Val	Leu				
190								195						200					
gtc	acc	atc	atc	ttc	atc	tac	gag	aag	cgc	cgg	aag	ccc	gag	gac	gtc	782			
Val	Thr	Ile	Ile	Phe	Ile	Tyr	Glu	Lys	Arg	Arg	Lys	Pro	Glu	Asp	Val				
205								210						215					
ctg	gat	gat	gac	gac	gcc	ggc	tct	gca	ccc	ctg	aag	agc	agc	ggg	cag	830			
Leu	Asp	Asp	Asp	Asp	Ala	Gly	Ser	Ala	Pro	Leu	Lys	Ser	Ser	Gly	Gln				
220								225						230					
cac	cag	aat	gac	aaa	ggc	aag	aac	gtc	cgc	cag	agg	aac	tct	tcc		875			
His	Gln	Asn	Asp	Lys	Gly	Lys	Asn	Val	Arg	Gln	Arg	Asn	Ser	Ser					
235								240						245					
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catcatacac	ttcctttcttt				tttaaaaaaac				ttgggttttc				tcattccagg				attctgttcc		1055
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<211> 269
<212> PRT
<213> Homo sapiens
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<222> 1..21
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-5				1					5					10		
Leu	Gly	Ser	Lys	Ile	Leu	Leu	Thr	Cys	Ser	Leu	Asn	Asp	Ser	Ala	Thr	
			15					20					25			
Glu	Val	Thr	Gly	His	Arg	Trp	Leu	Lys	Gly	Gly	Val	Val	Leu	Lys	Glu	
		30					35					40				
Asp	Ala	Leu	Pro	Gly	Gln	Lys	Thr	Glu	Phe	Lys	Val	Asp	Ser	Asp	Asp	
	45					50					55					
Gln	Trp	Gly	Glu	Tyr	Ser	Cys	Val	Phe	Leu	Pro	Glu	Pro	Met	Gly	Thr	
60					65					70					75	
Ala	Asn	Ile	Gln	Leu	His	Gly	Pro	Pro	Arg	Val	Lys	Ala	Val	Lys	Ser	



				80					85					90		
Ser	Glu	His	Ile	Asn	Glu	Gly	Glu	Thr	Ala	Met	Leu	Val	Cys	Lys	Ser	
			95					100					105			
Glu	Ser	Val	Pro	Pro	Val	Thr	Asp	Trp	Ala	Trp	Tyr	Lys	Ile	Thr	Asp	
		110					115					120				
Ser	Glu	Asp	Lys	Ala	Leu	Met	Asn	Gly	Ser	Glu	Ser	Arg	Phe	Phe	Val	
		125					130					135				
Ser	Ser	Ser	Gln	Gly	Leu	Ser	Glu	Leu	His	Ile	Glu	Asn	Leu	Asn	Met	
140					145					150					155	
Glu	Ala	Asp	Pro	Gly	Gln	Tyr	Arg	Cys	Asn	Gly	Thr	Ser	Ser	Lys	Gly	
			160						165					170		
Ser	Asp	Gln	Ala	Ile	Ile	Thr	Leu	Arg	Val	Arg	Ser	His	Leu	Ala	Ala	
			175					180					185			
Leu	Trp	Pro	Phe	Leu	Gly	Ile	Val	Ala	Glu	Val	Leu	Val	Leu	Val	Thr	
		190					195					200				
Ile	Ile	Phe	Ile	Tyr	Glu	Lys	Arg	Arg	Lys	Pro	Glu	Asp	Val	Leu	Asp	
		205				210					215					
Asp	Asp	Asp	Ala	Gly	Ser	Ala	Pro	Leu	Lys	Ser	Ser	Gly	Gln	His	Gln	
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<222> 1..343
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His	Cys	Gly	Glu	Gln	Leu	Glu	Cys	Arg	Leu	Asp	Thr	Gly	Gly	Asp	Leu	
			75					80					85			
agc	cgc	gga	gag	gtg	ccg	gaa	cct	ctg	tgt	gcc	tgt	cgt	tcg	cag	agt	739
Ser	Arg	Gly	Glu	Val	Pro	Glu	Pro	Leu	Cys	Ala	Cys	Arg	Ser	Gln	Ser	
		90					95					100				
ccg	ctc	tgc	ggg	tcc	gac	ggg	cac	acc	tac	tcc	cag	atc	tgc	cgc	ctg	787
Pro	Leu	Cys	Gly	Ser	Asp	Gly	His	Thr	Tyr	Ser	Gln	Ile	Cys	Arg	Leu	
	105					110					115					
cag	gag	gcg	gcc	cgc	gct	cgg	ccc	gat	gcc	aac	ctc	act	gtg	gca	cac	835
Gln	Glu	Ala	Ala	Arg	Ala	Arg	Pro	Asp	Ala	Asn	Leu	Thr	Val	Ala	His	
120					125				130						135	
ccg	ggg	ccc	tgc	gaa	tcg	ggg	ccc	cag	atc	gtg	tca	cat	cca	tat	gac	883
Pro	Gly	Pro	Cys	Glu	Ser	Gly	Pro	Gln	Ile	Val	Ser	His	Pro	Tyr	Asp	
			140					145					150			
act	tgg	aat	gtg	aca	ggg	cag	gat	gtg	atc	ttt	ggc	tgt	gaa	gtg	ttt	931
Thr	Trp	Asn	Val	Thr	Gly	Gln	Asp	Val	Ile	Phe	Gly	Cys	Glu	Val	Phe	
			155				160					165				
gcc	tac	ccc	atg	gcc	tcc	atc	gag	tgg	agg	aag	gat	ggc	ttg	gac	atc	979
Ala	Tyr	Pro	Met	Ala	Ser	Ile	Glu	Trp	Arg	Lys	Asp	Gly	Leu	Asp	Ile	
		170					175					180				
cag	ctg	cca	ggg	gat	gac	ccc	cac	atc	tct	gtg	cag	ttt	agg	ggg	gga	1027
Gln	Leu	Pro	Gly	Asp	Asp	Pro	His	Ile	Ser	Val	Gln	Phe	Arg	Gly	Gly	
	185					190					195					
ccc	cag	agg	ttt	gag	gtg	act	ggc	tgg	ctg	cag	atc	cag	gct	gtg	cgt	1075
Pro	Gln	Arg	Phe	Glu	Val	Thr	Gly	Trp	Leu	Gln	Ile	Gln	Ala	Val	Arg	
200					205				210					215		
ccc	agt	gat	gag	ggc	act	tac	cgc	tgc	ctt	ggc	cca	atg	ccc	tgg	gtc	1123
Pro	Ser	Asp	Glu	Gly	Thr	Tyr	Arg	Cys	Leu	Gly	Pro	Met	Pro	Trp	Val	
			220					225				230				
aag	tgg	agg	ccc	ctg	cta	gct	tgacagt	tgct	cacac	ctgac	cagctga	act				1174
Lys	Trp	Arg	Pro	Leu	Leu	Ala										
			235													
ctacagg	cat	cccc	cagctg	cgat	cactaa	acctg	gttcc	tgagg	aggag	gctg	agagtg					1234
aagaga	aatga	cgatt	actac	taggt	ccaga	gctct	ggccc	atggg	ggtgg	gtgag	cggct					1294
atagt	gttca	tccct	gctct	tgaaa	agacc	tgaaa	agggg	agcag	gggtcc	cttc	atcgac					1354
tgcttt	catg	ctgct	agtag	ggat	gatcat	gggag	gccta	tttg	actcca	aggt	agcagt					1414
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<212> PRT
<213> Homo sapiens
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<222> 1..30
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				-10					-5					1	
Ser	Pro	Gly	Pro	Asp	Tyr	Leu	Arg	Arg	Gly	Trp	Met	Arg	Leu	Leu	Ala
		5					10					15			
Glu	Gly	Glu	Gly	Cys	Ala	Pro	Cys	Arg	Pro	Glu	Glu	Cys	Ala	Ala	Pro
	20					25					30				
Arg	Gly	Cys	Leu	Ala	Gly	Arg	Val	Arg	Asp	Ala	Cys	Gly	Cys	Cys	Trp
35					40				45						50
Glu	Cys	Ala	Asn	Leu	Glu	Gly	Gln	Leu	Cys	Asp	Leu	Asp	Pro	Ser	Ala
				55					60					65	

His Phe Tyr Gly His Cys Gly Glu Gln Leu Glu Cys Arg Leu Asp Thr  
70 75 80  
Gly Gly Asp Leu Ser Arg Gly Glu Val Pro Glu Pro Leu Cys Ala Cys  
85 90 95  
Arg Ser Gln Ser Pro Leu Cys Gly Ser Asp Gly His Thr Tyr Ser Gln  
100 105 110  
Ile Cys Arg Leu Gln Glu Ala Ala Arg Ala Arg Pro Asp Ala Asn Leu  
115 120 125 130  
Thr Val Ala His Pro Gly Pro Cys Glu Ser Gly Pro Gln Ile Val Ser  
135 140 145  
His Pro Tyr Asp Thr Trp Asn Val Thr Gly Gln Asp Val Ile Phe Gly  
150 155 160  
Cys Glu Val Phe Ala Tyr Pro Met Ala Ser Ile Glu Trp Arg Lys Asp  
165 170 175  
Gly Leu Asp Ile Gln Leu Pro Gly Asp Asp Pro His Ile Ser Val Gln  
180 185 190  
Phe Arg Gly Gly Pro Gln Arg Phe Glu Val Thr Gly Trp Leu Gln Ile  
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Gln Ala Val Arg Pro Ser Asp Glu Gly Thr Tyr Arg Cys Leu Gly Pro  
215 220 225  
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230 235

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<212> DNA  
<213> Homo sapiens

<220>  
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<222> 1..26

<220>  
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<222> 27..689

<220>  
<221> 3'UTR  
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<220>  
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<220>  
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<222> 1325..1406

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GlyLeuArgAlaLeuCysArgValLeuLeuPheLeuSerGlnPheCys  
-20 -15 -10  
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-5 1 5 10  
tgtccgagcaaatggtttgtgtagcaggcttcctgcaaacgtgtatagac197  
CysProSerAsnGlyLeuCysSerArgLeuProAlaAspCysIleAsp  
15 20 25  
tgcaacaacaataatctctccgtgtaccattgggaagcctgtcacttttgac245  
CysThrThrAsnPheSerCysThrTyrGlyLysProValThrPheAsp

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tgt gca gtg aaa cca tct gtt acc	tgt gtt gat caa gac ttc aaa tcc	293	
Cys Ala Val Lys Pro Ser Val Thr	Cys Val Asp Gln Asp Phe Lys Ser		
45	50	55	
caa aag aac ttc atc att aac atg act	tgc aga ttt tgc tgg cag ctt	341	
Gln Lys Asn Phe Ile Ile Asn Met Thr	Cys Arg Phe Cys Trp Gln Leu		
60	65	70	
cct gaa aca gat tac gag tgt acc aac tcc	acc agc tgc atg acg gtg	389	
Pro Glu Thr Asp Tyr Glu Cys Thr Asn Ser	Thr Ser Cys Met Thr Val		
75	80	85	90
tcc tgt cct cgg cag cgc tac cct gcc aac	tgc acg gtg cgg gac cac	437	
Ser Cys Pro Arg Gln Arg Tyr Pro Ala Asn	Cys Thr Val Arg Asp His		
95	100	105	
gtc cac tgc ttg ggt aac cgt act ttt ccc	aaa atg cta tat tgc aat	485	
Val His Cys Leu Gly Asn Arg Thr Phe Pro	Lys Met Leu Tyr Cys Asn		
110	115	120	
tgg act gga ggc tat aag tgg tct acg gct	ctg gct cta agc atc acc	533	
Trp Thr Gly Tyr Lys Trp Ser Thr Ala Leu	Ala Leu Ser Ile Thr		
125	130	135	
ctc ggt ggg ttt gga gca gac cgt ttc tac	ctg ggc cag tgg cgg gaa	581	
Leu Gly Gly Phe Gly Ala Asp Arg Phe Tyr	Leu Gly Gln Trp Arg Glu		
140	145	150	
ggc ctc ggc aag ctc ttc agc ttc ggt ggc	ctg gga ata tgg acg ctg	629	
Gly Leu Gly Lys Leu Phe Ser Phe Gly Gly	Gly Ile Trp Thr Leu		
155	160	165	170
ata gac gtc ctg ctc att gga gtt ggc tat	ggt gga cca gca gat ggc	677	
Ile Asp Val Leu Leu Ile Gly Val Gly Tyr	Val Gly Pro Ala Asp Gly		
175	180	185	
tct ttg tac att tagctgtggt gtgtgcttca	gaaaggagca gggcttagaa	729	
Ser Leu Tyr Ile			
190			
aaagcccttt tgtccgtagg agttgatgtg	gtgtgagtga tatatttcta tgtttttaat	789	
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<220>  
 <221> SIGNAL  
 <222> 1..32

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 Thr Glu Ile Pro Pro Tyr Val Met Lys Cys Pro Ser Asn Gly Leu Cys  
 1 5 10 15  
 Ser Arg Leu Pro Ala Asp Cys Ile Asp Cys Thr Thr Asn Phe Ser Cys  
 20 25 30  
 Thr Tyr Gly Lys Pro Val Thr Phe Asp Cys Ala Val Lys Pro Ser Val



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 Arg Phe Arg Arg Trp Asn Cys Ser Ser His Ser Lys Ala Phe Gly Arg  
 60 65 70  
 atc ctg caa cag ggt cag tgt ggg gag ggg cac cct gca agg acc ctg 453  
 Ile Leu Gln Gln Gly Gln Cys Gly Glu Gly His Pro Ala Arg Thr Leu  
 75 80 85  
 cct ccc agg ccc ctg ggg cag ccc tcc cgc cgc agg ttt cag gtc cca 501  
 Pro Pro Arg Pro Leu Gly Gln Pro Ser Arg Arg Arg Phe Gln Val Pro  
 90 95 100 105  
 ggc ccc agc tgaccgcccc agccccgcgt gattgcacct gtctgcattc 550  
 Gly Pro Ser  
 acagacattc gggagacggc cttcgtgttc gccatcactg cggccggcgc cagccacgcc 610  
 gtcacgcagg cctgttctat gggcgagctg ctgcagtgcg gctgccaggc gccccgcggg 670  
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 <212> PRT  
 <213> Homo sapiens

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 <221> SIGNAL  
 <222> 1..24

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 -5 1 5  
 Leu Val Met Asp Pro Thr Ser Ile Cys Arg Lys Ala Arg Arg Leu Ala  
 10 15 20  
 Gly Arg Gln Ala Glu Leu Cys Gln Ala Glu Pro Glu Val Val Ala Glu  
 25 30 35 40  
 Leu Ala Arg Gly Ala Arg Leu Gly Val Arg Glu Cys Gln Phe Gln Phe  
 45 50 55  
 Arg Phe Arg Arg Trp Asn Cys Ser Ser His Ser Lys Ala Phe Gly Arg  
 60 65 70  
 Ile Leu Gln Gln Gly Gln Cys Gly Glu Gly His Pro Ala Arg Thr Leu  
 75 80 85  
 Pro Pro Arg Pro Leu Gly Gln Pro Ser Arg Arg Arg Phe Gln Val Pro  
 90 95 100  
 Gly Pro Ser  
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<210> 85

<211> 1754  
 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> 1..117

<220>  
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 <222> 118..510

<220>  
 <221> 3'UTR  
 <222> 511..1754

<220>  
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 <222> 1718..1723

<220>  
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 <222> 1739..1754

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 atg ctg ccg ccc tta ccc tcc cgc ctc ggg ctg ctg ctg ctg ctg 165  
 Met Leu Pro Pro Leu Pro Ser Arg Leu Gly Leu Leu Leu Leu Leu Leu  
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 ctg tgc ccg gcg cac gtc ggc gga ctg tgg tgg gct gtg ggc agc ccc 213  
 Leu Cys Pro Ala His Val Gly Gly Leu Trp Trp Ala Val Gly Ser Pro  
 -5 1 5  
 ttg gtt atg gac cct acc agc atc tgc agg aag gca cgg cgg ctg gcc 261  
 Leu Val Met Asp Pro Thr Ser Ile Cys Arg Lys Ala Arg Arg Leu Ala  
 10 15 20 25  
 ggg cgg cag gcc gag ttg tgc cag gct gag ccg gaa gtg gtg gca gag 309  
 Gly Arg Gln Ala Glu Leu Cys Gln Ala Glu Pro Glu Val Val Ala Glu  
 30 35 40  
 ctg gct cgg ggc gcc cgg ctc ggg gtg cga gag tgc cag ttc cag ttc 357  
 Leu Ala Arg Gly Ala Arg Leu Gly Val Arg Glu Cys Gln Phe Gln Phe  
 45 50 55  
 cgc ttc cgc cgc tgg aat tgc tcc agc cac agc aag gcc ttt gga cgc 405  
 Arg Phe Arg Arg Trp Asn Cys Ser Ser His Ser Lys Ala Phe Gly Arg  
 60 65 70  
 atc ctg caa cag ggt cag tgt ggg gag ggg cac cct gca agg acc ctg 453  
 Ile Leu Gln Gln Gly Gln Cys Gly Glu Gly His Pro Ala Arg Thr Leu  
 75 80 85  
 cct ccc agg ccc ctg ggg cag ccc tcc cgc cgc agg ttt cag gtc cca 501  
 Pro Pro Arg Pro Leu Gly Gln Pro Ser Arg Arg Arg Phe Gln Val Pro  
 90 95 100 105  
 ggc ccc agc tgaccgcccc agcccgcgct gattgcacct gtctgcattc 550  
 Gly Pro Ser  
 acagacattc gggagacggc cttcgtgttc gccatcactg cggccggcgc cagccacgcc 610  
 gtcacgcagg cctgttctat gggcgagctg ctgcagtgcg gctgccaggc gccccgcggg 670  
 cgggccccctc cccggccctc cggcctgccc ggcacccccg gacccccctg ccccgcgggc 730  
 tccccggaag gcagcgcgcg ctgggagtg gaggctgcg gcgacgacgt ggacttcggg 790  
 gacgagaagt cgaggctctt tatggacgcg cggcacaagc ggggacgcgg agacatccgc 850  
 gcgttggtgc aactgcacaa caacgaggcg ggcaggctgg ccgtgcggag ccacacgcgc 910  
 accgagtgc aatgccacgg gctgtcggga tcatgcgcgc tgcgcacctg ctggcagaag 970  
 ctgcctccat ttcgcgaggt gggcgcgcgg ctgctggagc gcttycacgg cgcctcacgc 1030  
 gtcatgggca ccaacgacgg caaggccctg ctgcccgcgg tccgcacgct caagccgccg 1090  
 ggccgagcgg acctcctcta cgccgcccgat tcgcccgaact tctgcgcccc caaccgacgc 1150

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accggctccc ccggcacgcg cggtcgcgcc tgcaatagca gcgccccgga cctcagcggc 1210
tgcgacctgc tgtgctgcgg ccgcgggcac cgccaggaga gcgtgcagct cgaagagaac 1270
tgctgtgcc gcttccactg gtgctgcgta gtacagtgcc accgctgccg tgtgcgcaag 1330
gagctcagcc tctgctgtg acccgccgcc cggccgctag actgacttcg cgcagcgggtg 1390
gctcgcacct gtgggacctc agggcaccgg caccgggcgc ctctcgccgc tcgagcccag 1450
cctctccctg ccaaagccca actcccaggg ctctggaaat ggtgaggcga ggggcttgag 1510
aggaacgccc acccacgaag gcccagggcg ccagacggcc ccgaaaaggc gctcggggag 1570
cgttttaaagg acactgtaca ggccctccct ccccttggcc tctaggagga aacagttttt 1630
tagactggaa aaaagccagt ctaaaggcct ctggatactg ggctccccag aactgctggc 1690
cacaggatgg tgggtgaggt tagtatcaat aaagatatatt aaaccaccaa aaaaaaaaaa 1750
aaaa

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<210> 86  
 <211> 131  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> 1..24

<400> 86

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				-20					-15						-10	
Leu	Cys	Pro	Ala	His	Val	Gly	Gly	Leu	Trp	Trp	Ala	Val	Gly	Ser	Pro	
			-5					1				5				
Leu	Val	Met	Asp	Pro	Thr	Ser	Ile	Cys	Arg	Lys	Ala	Arg	Arg	Leu	Ala	
	10					15					20					
Gly	Arg	Gln	Ala	Glu	Leu	Cys	Gln	Ala	Glu	Pro	Glu	Val	Val	Ala	Glu	
	25				30					35					40	
Leu	Ala	Arg	Gly	Ala	Arg	Leu	Gly	Val	Arg	Glu	Cys	Gln	Phe	Gln	Phe	
			45						50					55		
Arg	Phe	Arg	Arg	Trp	Asn	Cys	Ser	Ser	His	Ser	Lys	Ala	Phe	Gly	Arg	
			60					65					70			
Ile	Leu	Gln	Gln	Gly	Gln	Cys	Gly	Glu	Gly	His	Pro	Ala	Arg	Thr	Leu	
		75					80					85				
Pro	Pro	Arg	Pro	Leu	Gly	Gln	Pro	Ser	Arg	Arg	Arg	Phe	Gln	Val	Pro	
	90					95					100					
Gly	Pro	Ser														
	105															

<210> 87  
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 <212> DNA  
 <213> Homo sapiens

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<220>  
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 <222> 152..655

<220>  
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<220>  
 <221> polyA\_signal  
 <222> 1399..1404

<220>



<221> polyA\_site

<222> 1416..1431

<400> 87

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gccccaaacca aggcccccag agagggtcccc caggccccctt tgggtccctg agcctcagct 120  
ggagatccgg cgcaggagac caacgcctgc c atg ctg ttc cgg ctc tca gag 172  
Met Leu Phe Arg Leu Ser Glu

1 5  
cac tcc tca cca gag gag gaa gcc tcc ccc cac cag aga gcc tca gga 220  
His Ser Ser Pro Glu Glu Glu Ala Ser Pro His Gln Arg Ala Ser Gly

10 15 20  
gag ggg cac cat ctc aag tcg aag aga ccc aac ccc tgt gcc tac aca 268  
Glu Gly His His Leu Lys Ser Lys Arg Pro Asn Pro Cys Ala Tyr Thr

25 30 35  
cca cct tcg ctg aaa gct gtg cag cgc att gct gag tct cac ctg cag 316  
Pro Pro Ser Leu Lys Ala Val Gln Arg Ile Ala Glu Ser His Leu Gln

40 45 50 55  
tct atc agc aat ttg aat gag aac cag gcc tca gag gag gag gat gag 364  
Ser Ile Ser Asn Leu Asn Glu Asn Gln Ala Ser Glu Glu Glu Asp Glu

60 65 70  
ctg ggg gag ctt cgg gag ctg ggt tat cca aga gag gaa gat gag gag 412  
Leu Gly Glu Leu Arg Glu Leu Gly Tyr Pro Arg Glu Glu Asp Glu Glu

75 80 85  
gaa gag gag gat gat gaa gaa gag gaa gaa gaa gag gac agc cag gct 460  
Glu Glu Glu Asp Asp Glu Glu Glu Glu Glu Glu Asp Ser Gln Ala

90 95 100  
gaa gtc ctg aag gtc atc agg cag tct gct ggg caa aag aca acc tgt 508  
Glu Val Leu Lys Val Ile Arg Gln Ser Ala Gly Gln Lys Thr Thr Cys

105 110 115  
ggc cag ggt ctg gaa ggg ccc tgg gag cgc cca ccc cct ctg gat gag 556  
Gly Gln Gly Leu Glu Gly Pro Trp Glu Arg Pro Pro Pro Leu Asp Glu

120 125 130 135  
tcc gag aga gat gga ggc tct gag gac caa gtg gaa gac cca gca cta 604  
Ser Glu Arg Asp Gly Gly Ser Glu Asp Gln Val Glu Asp Pro Ala Leu

140 145 150  
agt gag cct ggg gag gaa cct cag cgc cct tcc ccc tct gag cct ggc 652  
Ser Glu Pro Gly Glu Glu Pro Gln Arg Pro Ser Pro Ser Glu Pro Gly

155 160 165  
aca taggcaccca gcctgcatct cccaggagga agtggagggg acatcgctgt 705  
Thr

tccccagaaa cccactctat cctcacccctg ttttgtgctc ttccctctgc ctgctagggc 765

tgccggttct gacttctaga agactaaggc tgggtctgtgt ttgcttgttt gccaccttt 825

ggctgatacc cagagaacct gggcacttgc tgccctgatgc ccaccctgc cagtcattcc 885

tccattcacc cagcgggagg tgggatgtga gacagcccac attggaaaat ccagaaaacc 945

gggaacaggg atttgccctt cacaattcta ctccccagat cctctccctt ggacacagga 1005

gaccacaggg gcaggaccct aagatctggg gaaaggaggt cctgagaacc ttgaggtacc 1065

cttagatcct tttctacca ctttccctat gaggattcca agtcaccact tctctcaccg 1125

gcttctacca ggggtccagga ctaaggcggt tttctccata gcctcaacat tttgggaatc 1185

ttcccttaat cacccttgct cctcctgggt gcctggaaga tggactggca gagacctctt 1245

tggtgcgttt tgtgctttga tgccaggaat gccgcctagt ttatgtcccc ggtggggcac 1305

acagcggggg gcgccaggtt ttccttgctc cccagctgct ctgccccctt ccccttcttc 1365

cctgactcca ggccctgaacc cctcccgtgc tgtaataaat ctttgtaaag aaaaaaaaaa 1425

aaaaaa 1431

<210> 88

<211> 168

<212> PRT

<213> Homo sapiens

<400> 88

Met Leu Phe Arg Leu Ser Glu His Ser Ser Pro Glu Glu Glu Ala Ser  
1 5 10 15

Pro His Gln Arg Ala Ser Gly Glu Gly His His Leu Lys Ser Lys Arg  
20 25 30  
Pro Asn Pro Cys Ala Tyr Thr Pro Pro Ser Leu Lys Ala Val Gln Arg  
35 40 45  
Ile Ala Glu Ser His Leu Gln Ser Ile Ser Asn Leu Asn Glu Asn Gln  
50 55 60  
Ala Ser Glu Glu Glu Asp Glu Leu Gly Glu Leu Arg Glu Leu Gly Tyr  
65 70 75 80  
Pro Arg Glu Glu Asp Glu Glu Glu Glu Asp Asp Glu Glu Glu Glu  
85 90 95  
Glu Glu Glu Asp Ser Gln Ala Glu Val Leu Lys Val Ile Arg Gln Ser  
100 105 110  
Ala Gly Gln Lys Thr Thr Cys Gly Gln Gly Leu Glu Gly Pro Trp Glu  
115 120 125  
Arg Pro Pro Pro Leu Asp Glu Ser Glu Arg Asp Gly Gly Ser Glu Asp  
130 135 140  
Gln Val Glu Asp Pro Ala Leu Ser Glu Pro Gly Glu Glu Pro Gln Arg  
145 150 155 160  
Pro Ser Pro Ser Glu Pro Gly Thr  
165

<210> 89  
<211> 1431  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> 1..151

<220>  
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<222> 152..655

<220>  
<221> 3'UTR  
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<220>  
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<222> 1399..1404

<220>  
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<222> 1416..1431

<400> 89  
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gcccaaacca aggcccccag agaggtcccc caggcccctt tgggtccctg agcctcagct 120  
ggagatccgg cgcaggagac caacgcctgc c atg ctg ttc cgg ctc tca gag 172  
Met Leu Phe Arg Leu Ser Glu  
1 5  
cac tcc tca cca gag gag gaa gcc tcc ccc cac cag aga gcc tca gga 220  
His Ser Ser Pro Glu Glu Glu Ala Ser Pro His Gln Arg Ala Ser Gly  
10 15 20  
gag ggg cac cat ctc aag tcg aag aga ccc aac ccc tgt gcc tac aca 268  
Glu Gly His His Leu Lys Ser Lys Arg Pro Asn Pro Cys Ala Tyr Thr  
25 30 35  
cca cct tcg ctg aaa gct gtg cag cgc att gct gag tct cac ctg cag 316  
Pro Pro Ser Leu Lys Ala Val Gln Arg Ile Ala Glu Ser His Leu Gln  
40 45 50 55  
tct atc agc aat ttg aat gag aac cag gcc tca gag gag gag gat gag 364  
Ser Ile Ser Asn Leu Asn Glu Asn Gln Ala Ser Glu Glu Glu Asp Glu

ctg ggg gag ctt cgg gag ctg ggt tat cca aga gag gaa gat gag gag	60	65	70	412
Leu Gly Glu Leu Arg Glu Leu Gly Tyr Pro Arg Glu Glu Asp Glu Glu				
75	80	85		
gaa gag gag gat gat gaa gaa gag gaa gaa gaa gag gac agc cag gct				460
Glu Glu Glu Asp Asp Glu Glu Glu Glu Glu Glu Glu Asp Ser Gln Ala				
90	95	100		
gaa gtc ctg aag gtc atc agg cag tct gct ggg caa aag aca acc tgt				508
Glu Val Leu Lys Val Ile Arg Gln Ser Ala Gly Gln Lys Thr Thr Cys				
105	110	115		
ggc cag ggt ctg gaa ggg ccc tgg gag cgc cca ccc cct ctg gat gag				556
Gly Gln Gly Leu Glu Gly Pro Trp Glu Arg Pro Pro Pro Leu Asp Glu				
120	125	130	135	
tcc gag aga gat gga ggc tct gag gac caa gtg gaa gac cca gca cta				604
Ser Glu Arg Asp Gly Gly Ser Glu Asp Gln Val Glu Asp Pro Ala Leu				
140	145	150		
agt gag cct ggg gag gaa cct cag cgc cct tcc ccc tct gag cct ggc				652
Ser Glu Pro Gly Glu Glu Pro Gln Arg Pro Ser Pro Ser Glu Pro Gly				
155	160	165		
aca taggcacca gcttgcattct cccaggagga agtggagggg acatcgctgt				705
Thr				
tccccagaaa cccactctat cctcaccctg ttttgtgtctc ttcccctcgc ctgctagggc				765
tgcggtttct gacttctaga agactaaggc tggctctgtgt ttgcttggtt gccaccttt				825
ggctgatacc cagagaacct gggcacttgc tgcctgatgc ccaccctgc cagtcattcc				885
tccattcacc cagcgggagg tgggatgtga gacagcccac attggaaaat ccagaaaacc				945
gggaacaggg atttgccctt cacaattcta ctccccagat cctctccctt ggacacagga				1005
gaccacaggg gcaggacct aagatctggg gaaaggaggt cctgagaacc ttgaggtacc				1065
cttagatcct tttctacca ctttcctatg gaggattcca agtcaccact tctctcaccg				1125
gcttctacca gggccagga ctaaggcgtt tttctccata gcctcaacat tttgggaatc				1185
ttcccttaat cacccttgct cctcctgggt gcctggaaga tggactggca gagacctctt				1245
tggttgcgttt tgtgctttga tgccaggaat gccgcctagt ttatgtcccc ggtggggcac				1305
acageggggg gcgccaggtt ttccttgctc cccagctgct ctgcccctt ccccttcttc				1365
cctgactcca ggccgaacc cctcccgtgc tgtaataaat ctttgtaaag aaaaaaaaaa				1425
aaaaaa				1431

<210> 90  
 <211> 168  
 <212> PRT  
 <213> Homo sapiens

<400> 90  
 Met Leu Phe Arg Leu Ser Glu His Ser Ser Pro Glu Glu Glu Ala Ser  
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 Pro His Gln Arg Ala Ser Gly Glu Gly His His Leu Lys Ser Lys Arg  
 20 25 30  
 Pro Asn Pro Cys Ala Tyr Thr Pro Pro Ser Leu Lys Ala Val Gln Arg  
 35 40 45  
 Ile Ala Glu Ser His Leu Gln Ser Ile Ser Asn Leu Asn Glu Asn Gln  
 50 55 60  
 Ala Ser Glu Glu Glu Asp Glu Leu Gly Glu Leu Arg Glu Leu Gly Tyr  
 65 70 75 80  
 Pro Arg Glu Glu Asp Glu Glu Glu Glu Glu Asp Asp Glu Glu Glu Glu  
 85 90 95  
 Glu Glu Glu Asp Ser Gln Ala Glu Val Leu Lys Val Ile Arg Gln Ser  
 100 105 110  
 Ala Gly Gln Lys Thr Thr Cys Gly Gln Gly Leu Glu Gly Pro Trp Glu  
 115 120 125  
 Arg Pro Pro Pro Leu Asp Glu Ser Glu Arg Asp Gly Gly Ser Glu Asp  
 130 135 140  
 Gln Val Glu Asp Pro Ala Leu Ser Glu Pro Gly Glu Glu Pro Gln Arg  
 145 150 155 160  
 Pro Ser Pro Ser Glu Pro Gly Thr  
 165

<210> 91  
 <211> 1417  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> 5'UTR  
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<220>  
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 <222> 48..1301

<220>  
 <221> 3'UTR  
 <222> 1302..1417

<220>  
 <221> polyA\_signal  
 <222> 1360..1365

<220>  
 <221> polyA\_site  
 <222> 1402..1417

<400> 91  
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 Met Pro Ser  
 tct gtc tcg tgg ggc atc ctc ctg ctg gca ggc ctg tgc tgc ctg gtc 104  
 Ser Val Ser Trp Gly Ile Leu Leu Leu Ala Gly Leu Cys Cys Leu Val  
 -20 -15 -10 -5  
 cct gtc tcc ctg gct gag gat ccc cag gga gat gct gcc cag aag aca 152  
 Pro Val Ser Leu Ala Glu Asp Pro Gln Gly Asp Ala Ala Gln Lys Thr  
 1 5 10  
 gat aca tcc cac cat gat cag gat cac cca acc ttc aac aag atc acc 200  
 Asp Thr Ser His His Asp Gln Asp His Pro Thr Phe Asn Lys Ile Thr  
 15 20 25  
 ccc aac ctg gct gag ttc gcc ttc agc cta tac cgc cag ctg gca cac 248  
 Pro Asn Leu Ala Glu Phe Ala Phe Ser Leu Tyr Arg Gln Leu Ala His  
 30 35 40  
 cag tcc aac agc acc aat atc ttc ttc tcc cca gtg agc atc gct aca 296  
 Gln Ser Asn Ser Thr Asn Ile Phe Phe Ser Pro Val Ser Ile Ala Thr  
 45 50 55 60  
 gcc ttt gca atg ctc tcc ctg ggg acc aag gct gac act cac gat gaa 344  
 Ala Phe Ala Met Leu Ser Leu Gly Thr Lys Ala Asp Thr His Asp Glu  
 65 70 75  
 atc ctg gag agc ctg aat ttc aac ctc acg gag att ccg gag gct cag 392  
 Ile Leu Glu Ser Leu Asn Phe Asn Leu Thr Glu Ile Pro Glu Ala Gln  
 80 85 90  
 atc cat gaa ggc ttc cag gaa ctc ctc cgt acc ctc aac cag cca gac 440  
 Ile His Glu Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn Gln Pro Asp  
 95 100 105  
 agc cag ctc cag ctg acc acc ggc aat ggc ctg ttc ctc agc gag ggc 488  
 Ser Gln Leu Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu Ser Glu Gly  
 110 115 120  
 ctg aag cta gtg gat aag ttt ttg gag gat gtt aaa aag ttg tac cac 536  
 Leu Lys Leu Val Asp Lys Phe Leu Glu Asp Val Lys Lys Leu Tyr His  
 125 130 135 140  
 tca gaa gcc ttc act gtc aac ttc ggg gac acc gaa gag gcc aag aaa 584  
 Ser Glu Ala Phe Thr Val Asn Phe Gly Asp Thr Glu Glu Ala Lys Lys  
 145 150 155  
 cag atc aac gat tac gtg gag aag ggt act caa ggg aaa att gtg gat 632

Gln	Ile	Asn	Asp	Tyr	Val	Glu	Lys	Gly	Thr	Gln	Gly	Lys	Ile	Val	Asp	
160								165					170			
ttg	gtc	aag	gag	ctt	gac	aga	gac	aca	gtt	ttt	gct	ctg	gtg	aat	tac	680
Leu	Val	Lys	Glu	Leu	Asp	Arg	Asp	Thr	Val	Phe	Ala	Leu	Val	Asn	Tyr	
175							180					185				
atc	ttc	ttt	aaa	ggc	aaa	tgg	gag	aga	ccc	ttt	gaa	gtc	aag	gac	acc	728
Ile	Phe	Phe	Lys	Gly	Lys	Trp	Glu	Arg	Pro	Phe	Glu	Val	Lys	Asp	Thr	
190						195					200					
gag	gaa	gag	gac	ttc	cac	gtg	gac	cag	gcg	acc	acc	gtg	aag	gtg	cct	776
Glu	Glu	Glu	Asp	Phe	His	Val	Asp	Gln	Ala	Thr	Thr	Val	Lys	Val	Pro	
205				210					215						220	
atg	atg	aag	cgt	tta	ggc	atg	ttt	aac	atc	cag	cac	tgt	aag	aag	ctg	824
Met	Met	Lys	Arg	Leu	Gly	Met	Phe	Asn	Ile	Gln	His	Cys	Lys	Lys	Leu	
225								230						235		
tcc	agc	tggt	gtg	ctg	ctg	atg	aaa	tac	ctg	ggc	aat	gcc	acc	gcc	atc	872
Ser	Ser	Trp	Val	Leu	Leu	Met	Lys	Tyr	Leu	Gly	Asn	Ala	Thr	Ala	Ile	
240								245				250				
ttc	ttc	ctg	cct	gat	gag	ggg	aaa	cta	cag	cac	ctg	gaa	aat	gaa	ctc	920
Phe	Phe	Leu	Pro	Asp	Glu	Gly	Lys	Leu	Gln	His	Leu	Glu	Asn	Glu	Leu	
255							260					265				
acc	cac	gat	atc	atc	acc	aag	ttc	ctg	gaa	aat	gaa	gac	aga	agg	tct	968
Thr	His	Asp	Ile	Ile	Thr	Lys	Phe	Leu	Glu	Asn	Glu	Asp	Arg	Arg	Ser	
270						275					280					
gcc	agc	tta	cat	tta	ccc	aaa	ctg	tcc	att	act	gga	acc	tat	gat	ctg	1016
Ala	Ser	Leu	His	Leu	Pro	Lys	Leu	Ser	Ile	Thr	Gly	Thr	Tyr	Asp	Leu	
285				290					295						300	
aag	agc	gtc	ctg	ggc	caa	ctg	ggc	atc	act	aag	gtc	ttc	agc	aat	ggg	1064
Lys	Ser	Val	Leu	Gly	Gln	Leu	Gly	Ile	Thr	Lys	Val	Phe	Ser	Asn	Gly	
305								310						315		
gct	gac	ctc	tcc	ggg	gtc	aca	gag	gag	gca	ccc	ctg	aag	ctc	tcc	aag	1112
Ala	Asp	Leu	Ser	Gly	Val	Thr	Glu	Glu	Ala	Pro	Leu	Lys	Leu	Ser	Lys	
320								325					330			
gcc	gtg	cat	aag	gct	gtg	ctg	acc	atc	gac	gag	aaa	ggg	act	gaa	gct	1160
Ala	Val	His	Lys	Ala	Val	Leu	Thr	Ile	Asp	Glu	Lys	Gly	Thr	Glu	Ala	
335							340					345				
gct	ggg	gcc	atg	ttt	tta	gag	gcc	ata	ccc	atg	tct	atc	ccc	ccc	gag	1208
Ala	Gly	Ala	Met	Phe	Leu	Glu	Ala	Ile	Pro	Met	Ser	Ile	Pro	Pro	Glu	
350						355					360					
gtc	aag	ttc														

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<210> 92
<211> 418
<212> PRT
<213> Homo sapiens
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<220>  
<221> SIGNAL  
<222> 1..24
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Cys Leu Val Pro Val Ser Leu Ala Glu Asp Pro Gln Gly Asp Ala Ala  
-5 1 5  
Gln Lys Thr Asp Thr Ser His His Asp Gln Asp His Pro Thr Phe Asn  
10 15 20

Lys Ile Thr Pro Asn Leu Ala Glu Phe Ala Phe Ser Leu Tyr Arg Gln  
 25 30 35 40  
 Leu Ala His Gln Ser Asn Ser Thr Asn Ile Phe Phe Ser Pro Val Ser  
 45 50 55  
 Ile Ala Thr Ala Phe Ala Met Leu Ser Leu Gly Thr Lys Ala Asp Thr  
 60 65 70  
 His Asp Glu Ile Leu Glu Ser Leu Asn Phe Asn Leu Thr Glu Ile Pro  
 75 80 85  
 Glu Ala Gln Ile His Glu Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn  
 90 95 100  
 Gln Pro Asp Ser Gln Leu Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu  
 105 110 115 120  
 Ser Glu Gly Leu Lys Leu Val Asp Lys Phe Leu Glu Asp Val Lys Lys  
 125 130 135  
 Leu Tyr His Ser Glu Ala Phe Thr Val Asn Phe Gly Asp Thr Glu Glu  
 140 145 150  
 Ala Lys Lys Gln Ile Asn Asp Tyr Val Glu Lys Gly Thr Gln Gly Lys  
 155 160 165  
 Ile Val Asp Leu Val Lys Glu Leu Asp Arg Asp Thr Val Phe Ala Leu  
 170 175 180  
 Val Asn Tyr Ile Phe Phe Lys Gly Lys Trp Glu Arg Pro Phe Glu Val  
 185 190 195 200  
 Lys Asp Thr Glu Glu Glu Asp Phe His Val Asp Gln Ala Thr Thr Val  
 205 210 215  
 Lys Val Pro Met Met Lys Arg Leu Gly Met Phe Asn Ile Gln His Cys  
 220 225 230  
 Lys Lys Leu Ser Ser Trp Val Leu Leu Met Lys Tyr Leu Gly Asn Ala  
 235 240 245  
 Thr Ala Ile Phe Phe Leu Pro Asp Glu Gly Lys Leu Gln His Leu Glu  
 250 255 260  
 Asn Glu Leu Thr His Asp Ile Ile Thr Lys Phe Leu Glu Asn Glu Asp  
 265 270 275 280  
 Arg Arg Ser Ala Ser Leu His Leu Pro Lys Leu Ser Ile Thr Gly Thr  
 285 290 295  
 Tyr Asp Leu Lys Ser Val Leu Gly Gln Leu Gly Ile Thr Lys Val Phe  
 300 305 310  
 Ser Asn Gly Ala Asp Leu Ser Gly Val Thr Glu Glu Ala Pro Leu Lys  
 315 320 325  
 Leu Ser Lys Ala Val His Lys Ala Val Leu Thr Ile Asp Glu Lys Gly  
 330 335 340  
 Thr Glu Ala Ala Gly Ala Met Phe Leu Glu Ala Ile Pro Met Ser Ile  
 345 350 355 360  
 Pro Pro Glu Val Lys Phe Asn Lys Pro Phe Val Phe Leu Met Ile Glu  
 365 370 375  
 Gln Asn Thr Lys Ser Pro Leu Phe Met Gly Lys Val Val Asn Pro Thr  
 380 385 390  
 Gln Lys

<210> 93  
 <211> 1115  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> 5'UTR  
 <222> 1..277  
  
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 <221> CDS  
 <222> 278..733

<220>  
 <221> 3'UTR

<222> 734..1115

<220>

<221> polyA\_signal

<222> 1072..1077

<220>

<221> polyA\_site

<222> 1101..1115

<400> 93

ctctttgctc taacagacag cagcgacttt aggctggata atagtcaa at tcttacctcg 60  
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tcttgatctg cttctaaaag aagaagtaga gaagataaat cctgtcttca atacctggaa 180  
ggaaaaacaa aataacctca actccgtttt gaaaaaaaca ttccaagaac tttcatcaga 240  
gattttactt agatgattta cacaatgaag aaagtac atg cac ttt ggg ctt ctg 295  
Met His Phe Gly Leu Leu

-15

tcc ctg ctg ctt aat ctt gcc cct gcc cct ctt aat gct gat tct gag 343  
Ser Leu Leu Leu Asn Leu Ala Pro Ala Pro Leu Asn Ala Asp Ser Glu

-10

-5

1

gaa gat gaa gaa cac aca att atc aca gat acg gag ttg cca cca ctg 391  
Glu Asp Glu Glu His Thr Ile Ile Thr Asp Thr Glu Leu Pro Pro Leu

5

10

15

20

aaa ctt atg cat tca ttt tgt gca ttc aag gcg gat gat agc cca tgt 439  
Lys Leu Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp Ser Pro Cys

25

30

35

aaa gca atc atg aaa aga ttt ttc ttc aat att ttc act cga cag tgc 487  
Lys Ala Ile Met Lys Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys

40

45

50

gaa gaa ttt ata tat ggg gga tgt gaa gga aat cag aat cga ttt gaa 535  
Glu Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn Arg Phe Glu

55

60

65

agt ctg gaa gag tgc aaa aaa atg tgt aca aga gat aat gca aac agg 583  
Ser Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp Asn Ala Asn Arg

70

75

80

att ata aag aca aca ttg caa caa gaa aag cca gat ttc tgc ttt ttg 631  
Ile Ile Lys Thr Thr Leu Gln Gln Glu Lys Pro Asp Phe Cys Phe Leu

85

90

95

100

gaa gaa gat cct gga ata tgt cga ggt tat att acc agg tat ttt tat 679  
Glu Glu Asp Pro Gly Ile Cys Arg Gly Tyr Ile Thr Arg Tyr Phe Tyr

105

110

115

aac aat cag aca aaa cat gtg aac gtt tca agt atg gtg gat gcc tgg 727  
Asn Asn Gln Thr Lys His Val Asn Val Ser Ser Met Val Asp Ala Trp

120

125

130

gca ata tgaacaattt tgagacactg gaagaatgca agaacatttg tgaagatggt 783  
Ala Ile

ccgaatgggt tccaggtgga taattatgga acccagctca atgctgtgaa taactccctg 843  
actccgcaat caaccaaggt tcccagcctt tttgttaca aagaaggaa aaatgatggt 903  
tggaagaatg cggtcatat ttaccaagtc tttctgaacg ccttctgcat tcatgcatcc 963  
atgttctttc taggattgga tagcatttca tgccatgtt aatatttggt cttttggcat 1023  
ttccttaata tttatatgta tacgtgatgc ctttgatagc atactgctaa taaagtttta 1083  
atattttacat gcataggaaa aaaaaaaaaa aa 1115

<210> 94

<211> 152

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<213> Homo sapiens

<220>

<221> SIGNAL

<222> 1..19

[illegible]

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<222> 1269..1274
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ctcttttcact gctagtaaga tcagattgcg tttcttttccag ttactctttca atcgccagtt	120
tcttgatctg cttctaanaag aagaagtaga gaagataaat cctgtcttca atacctggaa	180
ggaaaaaacag aataacctca actccgTTTT gaaaaaaaaaaca ttccaagaac tttcatcaga	240
gatttttactt ag atg att tac acA atG aaG aaa gta cat gCA ctt tgg gct	291
Met Ile Tyr Thr Met Lys Lys Val His Ala Leu Trp Ala	
-25 -20 -15	
tct gta tgc ctg ctg ctt aat ctt gcc cct gcc cct ctt aat gct gat	339
Ser Val Cys Leu Leu Leu Asn Leu Ala Pro Ala Pro Leu Asn Ala Asp	
-10 -5 1	
tct gag gaa gat gaa gaa cac aca att atc aca gat acg gag ttg cca	387
Ser Glu Glu Asp Glu Glu His Thr Ile Ile Thr Asp Thr Glu Leu Pro	
5 10 15	
cca ctg aaa ctt atg cat tca ttt tgt gca ttc aag gcg gat gat ggc	435
Pro Leu Lys Leu Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp Gly	



20					25					30							
cca	tgt	aaa	gca	atc	atg	aaa	aga	ttt	ttc	ttc	aat	att	ttc	act	cga	483	
Pro	Cys	Lys	Ala	Ile	Met	Lys	Arg	Phe	Phe	Phe	Asn	Ile	Phe	Thr	Arg		
35					40					45					50		
cag	tgc	gaa	gaa	ttt	ata	tat	ggg	gga	tgt	gaa	gga	aat	cag	aat	cga	531	
Gln	Cys	Glu	Glu	Phe	Ile	Tyr	Gly	Gly	Cys	Glu	Gly	Asn	Gln	Asn	Arg		
55					60					65							
ttt	gaa	agt	ctg	gaa	gag	tgc	aaa	aaa	atg	tgt	aca	aga	gat	aat	gca	579	
Phe	Glu	Ser	Leu	Glu	Glu	Cys	Lys	Lys	Met	Cys	Thr	Arg	Asp	Asn	Ala		
70					75					80							
aac	agg	att	ata	aag	aca	aca	ttg	caa	caa	gaa	aag	cca	gat	ttc	tgc	627	
Asn	Arg	Ile	Ile	Lys	Thr	Thr	Leu	Gln	Gln	Glu	Lys	Pro	Asp	Phe	Cys		
85					90					95							
ttt	ttg	gaa	gaa	gat	cct	gga	ata	tgt	cga	ggt	tat	att	acc	agg	tat	675	
Phe	Leu	Glu	Glu	Asp	Pro	Gly	Ile	Cys	Arg	Gly	Tyr	Ile	Thr	Arg	Tyr		
100					105					110							
ttt	tat	aac	aat	cag	aca	aaa	cag	tgt	gaa	cgt	ttc	aag	tat	ggt	gga	723	
Phe	Tyr	Asn	Asn	Gln	Thr	Lys	Gln	Cys	Glu	Arg	Phe	Lys	Tyr	Gly	Gly		
115					120					125					130		
tgc	ctg	ggc	aat	caa	caa	ttt	tgagacactg	gaacaatgca	agaacatttg							774	
Cys	Leu	Gly	Asn	Gln	Gln	Phe											
135																	
tgaagatggt	ccgaatgggt	tccaggtgga	taattatgga	accagctca	atgctgtgaa	834											
taactccctg	actccgcaat	caaccaaggt	tcccagcctt	tttgaatttc	acggtcacctc	894											
atggtgtctc	actccagcag	acagaggatt	gtgtcgtgcc	aatgagaaca	gattctacta	954											
caattcagtc	attgggaaat	gccgccatt	taagtacagt	ggatgtgggg	gaaatgaaaa	1014											
caattttact	tccaaacaag	aatgtctgag	ggcatgtaaa	aaaggtttca	tccaaagaat	1074											
atcaaaagga	ggcctaatta	aaacccaaaag	aaaaagaaaag	aagcagagag	tgaaaatagc	1134											
atatgaagaa	attttttgta	aaaatatgtg	aattttgttat	agcaatgtaa	cattaattct	1194											
actaaatatt	ttatatgaaa	tgtttcacta	tgattttctca	tttttcttct	aaaatgcttt	1254											
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<210> 96
<211> 164
<212> PRT
<213> Homo sapiens
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<222> 1..28
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<220>  
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 <222> 118..504

<220>  
 <221> 3'UTR  
 <222> 505..1855

<220>  
 <221> polyA\_signal  
 <222> 1819..1824

<220>  
 <221> polyA\_site  
 <222> 1840..1855

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 atg ctg ccg ccc tta ccc tcc cgc ctc ggg ctg ctg ctg ctg ctg ctc 165  
 Met Leu Pro Pro Leu Pro Ser Arg Leu Gly Leu Leu Leu Leu Leu Leu  
 -20 -15 -10  
 ctg tgc ccg gcg cac gtc ggc gga ctg tgg tgg gct gtg ggc agc ccc 213  
 Leu Cys Pro Ala His Val Gly Gly Leu Trp Trp Ala Val Gly Ser Pro  
 -5 1 5  
 ttg gtt atg gac cct acc agc atc tgc agg aag gca cgg cgg ctg gcc 261  
 Leu Val Met Asp Pro Thr Ser Ile Cys Arg Lys Ala Arg Arg Leu Ala  
 10 15 20 25  
 ggg cgg cag gcc gag ttg tgc cag gct gag ccg gaa gtg gtg gca gag 309  
 Gly Arg Gln Ala Glu Leu Cys Gln Ala Glu Pro Glu Val Val Ala Glu  
 30 35 40  
 ctg gct cgg ggc gcc cgg ctc ggg gtg cga gag tgc cag ttc cag ttc 357  
 Leu Ala Arg Gly Ala Arg Leu Gly Val Arg Glu Cys Gln Phe Gln Phe  
 45 50 55  
 cgc ttc cgc cgc tgg aat tgc tcc agc cac agc aag gcc ttt gga cgc 405  
 Arg Phe Arg Arg Trp Asn Cys Ser Ser His Ser Lys Ala Phe Gly Arg  
 60 65 70  
 atc ctg caa cag ggt cag tgt ggg gag ggg gcg gaa gtg ggg ctg ctt 453  
 Ile Leu Gln Gln Gly Gln Cys Gly Glu Gly Ala Glu Val Gly Leu Leu  
 75 80 85  
 tct ccc tgc tgt ggg acc cga gga gag gag aac tgg ttc gct gaa gtt 501  
 Ser Pro Cys Cys Gly Thr Arg Gly Glu Glu Asn Trp Phe Ala Glu Val  
 90 95 100 105  
 gcc tgagccccac ttccccctca catgtgtctg ggcaccctgc aaggaccctg 554  
 Ala  
 cctcccaggc ccttggggca gccctccgc cgcagggttc aggtcccagg ccccagctga 614  
 ccgccccagc ccgcgctgat tgcacctgtc tgcattcaca gacattcggg agacggcctt 674  
 cgtgttcgcc atcactgcgg ccggcgccag ccacgcgcgc acgcaggcct gttctatggg 734  
 cgagctgctg cagtgcggct gccaggcgcc ccgcggggcg gccctcccc ggccctccgg 794  
 cctgcccggc acccccggac cccctggccc cgcgggctcc ccggaaggca gcgccgcctg 854  
 ggagtgggga ggctgcggcg acgacgtgga cttcggggac gagaagtcga ggctctttat 914  
 ggacgcgcgg cacaagcggg gacgcggaga catccgcgcg ttggtgcaac tgcacaacaa 974

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cgaggcgggc aggctggccg tgcggagcca caccgcgacc gagtgcaaat gccacgggct 1034
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cgcgcggtg ctggagcgct tccacggcgc ctcacgcgtc atgggcacca acgacggcaa 1154
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cctccctccc cttggcctct aggaggaaac agtttttttag actggaaaaa agccagtcta 1754
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tatcaataaa gatatttaaa ccaccaaaaa aaaaaaaaaa a 1855

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 <211> 129  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> 1..24

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 Leu Cys Pro Ala His Val Gly Gly Leu Trp Trp Ala Val Gly Ser Pro  
                   -5                  1                  5  
 Leu Val Met Asp Pro Thr Ser Ile Cys Arg Lys Ala Arg Arg Leu Ala  
   10                  15                  20  
 Gly Arg Gln Ala Glu Leu Cys Gln Ala Glu Pro Glu Val Val Ala Glu  
 25                  30                  35                  40  
 Leu Ala Arg Gly Ala Arg Leu Gly Val Arg Glu Cys Gln Phe Gln Phe  
                   45                  50                  55  
 Arg Phe Arg Arg Trp Asn Cys Ser Ser His Ser Lys Ala Phe Gly Arg  
                   60                  65                  70  
 Ile Leu Gln Gln Gly Gln Cys Gly Glu Gly Ala Glu Val Gly Leu Leu  
   75                  80                  85  
 Ser Pro Cys Cys Gly Thr Arg Gly Glu Glu Asn Trp Phe Ala Glu Val  
   90                  95                  100  
 Ala  
 105

<210> 99  
 <211> 667  
 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> 1..94

<220>  
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 <222> 95..613

<220>  
 <221> 3'UTR  
 <222> 614..667

<220>

<221> polyA\_signal

<222> 636..641

<220>

<221> polyA\_site

<222> 652..667

<400> 99

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gttccatctc aacagccctt gttttggaaa ggac atg att gtc aag ggg gtg gcc 115  
Met Ile Val Lys Gly Val Ala

1 5  
tcc aga act gtg gtt tcc aga ccg ttc ccc ggt aac tgg ctt ttc tct 163  
Ser Arg Thr Val Val Ser Arg Pro Phe Pro Gly Asn Trp Leu Phe Ser  
10 15 20

tcc atc cag ctg act gat gat cag ggc ccc gtc ctg atg acc act gta 211  
Ser Ile Gln Leu Thr Asp Asp Gln Gly Pro Val Leu Met Thr Thr Val  
25 30 35

gcc atg cct gtg ttt agt aag cag aac gaa acc aga tcg aag ggc att 259  
Ala Met Pro Val Phe Ser Lys Gln Asn Glu Thr Arg Ser Lys Gly Ile  
40 45 50 55

ctt ctg gga gtg gtt ggc aca gat gtc cca gtg aaa gaa ctt ctg aag 307  
Leu Leu Gly Val Val Gly Thr Asp Val Pro Val Lys Glu Leu Leu Lys  
60 65 70

acc atc ccc aaa tac aag tta ggg att cac ggt tat gcc ttt gca atc 355  
Thr Ile Pro Lys Tyr Lys Leu Gly Ile His Gly Tyr Ala Phe Ala Ile  
75 80 85

aca aat aat gga tat atc ctg acg cat ccg gaa ctc agg ctg ctg tac 403  
Thr Asn Asn Gly Tyr Ile Leu Thr His Pro Glu Leu Arg Leu Leu Tyr  
90 95 100

gaa gaa gga aaa aag cga agg aaa cct aac tat agt agc gtt gac ctc 451  
Glu Glu Gly Lys Lys Arg Arg Lys Pro Asn Tyr Ser Ser Val Asp Leu  
105 110 115

tct gag gtg gag tgg gaa gac cga gat gac gtg ttg aga aat gct atg 499  
Ser Glu Val Glu Trp Glu Asp Arg Asp Asp Val Leu Arg Asn Ala Met  
120 125 130 135

gtg aat cga aag acg ggg aag ttt tcc atg gag gtg aag aag aca gtg 547  
Val Asn Arg Lys Thr Gly Lys Phe Ser Met Glu Val Lys Lys Thr Val  
140 145 150

gac aaa ggg gta cat ttt tct caa aca ttt ttg ctg ctt aat tta aaa 595  
Asp Lys Gly Val His Phe Ser Gln Thr Phe Leu Leu Leu Asn Leu Lys  
155 160 165

caa acc act gtg aaa aat tagctttgaa agctatatct ggaataaata 643  
Gln Thr Thr Val Lys Asn  
170

tctttcgcaa aaaaaaaaaa aaaa 667

<210> 100

<211> 173

<212> PRT

<213> Homo sapiens

<400> 100

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20 25 30  
Pro Val Leu Met Thr Thr Val Ala Met Pro Val Phe Ser Lys Gln Asn  
35 40 45  
Glu Thr Arg Ser Lys Gly Ile Leu Leu Gly Val Val Gly Thr Asp Val  
50 55 60  
Pro Val Lys Glu Leu Leu Lys Thr Ile Pro Lys Tyr Lys Leu Gly Ile  
65 70 75 80

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<222> 1..153

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<221> 3'UTR
<222> 640..1062
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<222> 1047..1062
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93

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105						110					115					
acc	agc	atg	aag	gac	atg	cgc	aaa	gtt	ctg	aga	aca	tta	cag	cag	atc	558
Thr	Ser	Met	Lys	Asp	Met	Arg	Lys	Val	Leu	Arg	Thr	Leu	Gln	Gln	Ile	
120					125					130					135	
aag	aaa	tcc	agc	tca	aga	ggg	gac	aaa	cgc	cat	ttc	ctc	aac	tgg	cag	606
Lys	Lys	Ser	Ser	Ser	Arg	Gly	Asp	Lys	Arg	His	Phe	Leu	Asn	Trp	Gln	
				140					145					150		
aag	gga	ctg	aag	cct	ctc	cct	caa	gcc	ctt	tta	taggggtcct	cattgtcagg				659
Lys	Gly	Leu	Lys	Pro	Leu	Pro	Gln	Ala	Leu	Leu						
		155						160								
cctctaagcc	caagccaagc	catcgcatcc	cctgtgactt	gcacatatac	gcccagatgg											719
cctgaagtaa	ctgaagaatc	acaaaagaag	tgaaaaggcc	ctgcctcgcc	ttactgatg											779
acgttccacc	attgtgattt	gttcctgccc	caccttaact	gagtgattaa	ccctgtgaat											839
ttccttctcc	tggtctagaa	gctccccac	tgagcacctt	gtgacccctt	gcccctgccc											899
accagagaac	aacccccctt	gactgtaatt	ttccattacc	ttcccaaatac	ctataaaaacg											959
gccccacccc	tatctccctt	tgtgactct	cttttcggac	tcagcccacc	tgcagccagg											1019
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<210> 102  
 <211> 162  
 <212> PRT  
 <213> Homo sapiens

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Phe	Arg	Arg	Arg	Gln	Thr	Cys	Gln	Leu	Leu	Leu	Glu	Val	Ala	Trp	Pro	
			20					25					30			
Leu	Phe	Ile	Phe	Leu	Ile	Leu	Ile	Ser	Val	Arg	Leu	Ser	Tyr	Pro	Pro	
		35				40					45					
Tyr	Glu	Gln	His	Glu	Cys	His	Phe	Pro	Asn	Lys	Ala	Met	Pro	Ser	Ala	
	50				55						60					
Gly	Thr	Leu	Pro	Trp	Val	Gln	Gly	Ile	Ile	Cys	Asn	Ala	Asn	Asn	Pro	
65				70					75					80		
Cys	Phe	Arg	Tyr	Pro	Thr	Pro	Gly	Glu	Ala	Pro	Gly	Val	Val	Gly	Asn	
				85				90						95		
Phe	Asn	Lys	Ser	Ile	Val	Ala	Arg	Leu	Phe	Ser	Asp	Ala	Arg	Arg	Leu	
			100					105					110			
Leu	Leu	Tyr	Ser	Gln	Lys	Asp	Thr	Ser	Met	Lys	Asp	Met	Arg	Lys	Val	
		115					120					125				
Leu	Arg	Thr	Leu	Gln	Gln	Ile	Lys	Lys	Ser	Ser	Ser	Arg	Gly	Asp	Lys	
	130					135					140					
Arg	His	Phe	Leu	Asn	Trp	Gln	Lys	Gly	Leu	Lys	Pro	Leu	Pro	Gln	Ala	
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Leu	Leu															

<210> 103  
 <211> 933  
 <212> DNA  
 <213> Homo sapiens

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 <222> 1..149

<220>  
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 <222> 150..392

<220>  
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<222> 63..933

<400> 103

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cagatgtgta cggatgaaaa tacagtggag atg agt cag aaa ccg gcc aag gag 173
                               Met Ser Gln Lys Pro Ala Lys Glu
                               1           5
ggt ccc aga ctc tcc aaa aac cag aag tac tcc gaa cac ttc agc ata 221
Gly Pro Arg Leu Ser Lys Asn Gln Lys Tyr Ser Glu His Phe Ser Ile
10           15           20
cac tgc tgc ccg ccg ttc acc ttc ctc aat tcc aag aag gag ata gtg 269
His Cys Cys Pro Pro Phe Thr Phe Leu Asn Ser Lys Lys Glu Ile Val
25           30           35           40
gat cgg aaa tac agc atc tgt aag agc ggc tgc ttc tac cag aag aaa 317
Asp Arg Lys Tyr Ser Ile Cys Lys Ser Gly Cys Phe Tyr Gln Lys Lys
45           50           55
gag gag gac tgg atc tgc tgc gcc tgc cag aag acc aga ttg aaa agg 365
Glu Glu Asp Trp Ile Cys Cys Ala Cys Gln Lys Thr Arg Leu Lys Arg
60           65           70
aag atc agg cca acc cca aag aag aag tgaccaagga ggagtttaaa 412
Lys Ile Arg Pro Thr Pro Lys Lys Lys
75           80
ytgaatgaac aacctcggct cctggactca ttgcttcaca acccatctac ccctggatga 472
agttatctgg cttcaaatat tatgcagggg caaacacctg ctgatgtggc aactgctgat 532
gctcatggtc cccatggcat gggggcctca gggcagcctg cctggagtag tttgaagatg 592
tcattccatt gtcttctgac ctctataatt gccactgaga gatctgctgt cagtctgctt 652
atccttccac ggactcaagt ttcttcaatc tgaagataca tgtctttctc caaggacatg 712
tggaaaaaaaa aaagatgtta tacaaccatc aaagtggcaa aaataaaaaa aattggctgg 772
gcgtgggtggc gggcgctgt ggtcccagct actcgggagg ctgaggcagg agaatggcgt 832
gaacctggga ggcggagctt gcagtgcgc cactgcactc cagcctgggc 892
gacagagcga gactctgtct caaacaacaaa aaaaaaaaaa a 933
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<210> 104

<211> 81

<212> PRT

<213> Homo sapiens

<400> 104

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1           5           10           15
Lys Tyr Ser Glu His Phe Ser Ile His Cys Cys Pro Pro Phe Thr Phe
20           25           30
Leu Asn Ser Lys Lys Glu Ile Val Asp Arg Lys Tyr Ser Ile Cys Lys
35           40           45
Ser Gly Cys Phe Tyr Gln Lys Lys Glu Glu Asp Trp Ile Cys Cys Ala
50           55           60
Cys Gln Lys Thr Arg Leu Lys Arg Lys Ile Arg Pro Thr Pro Lys Lys
65           70           75           80
Lys
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<210> 105

<211> 1187

<212> DNA

<213> Homo sapiens

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<221> 5'UTR

<222> 1..34

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 <222> 35..1069

<220>  
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<220>  
 <221> polyA\_signal  
 <222> 1146..1151

<220>  
 <221> polyA\_site  
 <222> 1172..1187

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 Met Ile Ser Pro Val Leu Ile  
 -15

ttg ttc tcg agt ttt ctc tgc cat gtt gct att gca gga cgg acc tgt	103
Leu Phe Ser Ser Phe Leu Cys His Val Ala Ile Ala Gly Arg Thr Cys	
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ccc aag cca gat gat tta cca ttt tcc aca gtg gtc ccg tta aaa aca	151
Pro Lys Pro Asp Asp Leu Pro Phe Ser Thr Val Val Pro Leu Lys Thr	
10 15 20	
ttc tat gag cca gga gaa gag att acg tat tcc tgc aag ccg ggc tat	199
Phe Tyr Glu Pro Gly Glu Glu Ile Thr Tyr Ser Cys Lys Pro Gly Tyr	
25 30 35	
gtg tcc cga gga ggg atg aga aag ttt atc tgc cct ctc aca gga ctg	247
Val Ser Arg Gly Gly Met Arg Lys Phe Ile Cys Pro Leu Thr Gly Leu	
40 45 50	
tgg ctc atc aac act ctg aaa tgt aca ccc aga gta tgt cct ttt gct	295
Trp Leu Ile Asn Thr Leu Lys Cys Thr Pro Arg Val Cys Pro Phe Ala	
55 60 65	
gga atc tta gaa aat gga gcc gta cgc tat acg act ttt gaa tat ccc	343
Gly Ile Leu Glu Asn Gly Ala Val Arg Tyr Thr Thr Phe Glu Tyr Pro	
70 75 80 85	
aac acg atc agt ttt tct tgt aac act ggg ttt tat ctg aat ggc gct	391
Asn Thr Ile Ser Phe Ser Cys Asn Thr Gly Phe Tyr Leu Asn Gly Ala	
90 95 100	
gat tct gcc aag tgc act gag gaa gga aaa tgg agc ccg gag ctt cct	439
Asp Ser Ala Lys Cys Thr Glu Glu Gly Lys Trp Ser Pro Glu Leu Pro	
105 110 115	
gtc tgt gct ccc atc atc tgc cct cca cca tcc ata cct acg ttt gca	487
Val Cys Ala Pro Ile Ile Cys Pro Pro Pro Ser Ile Pro Thr Phe Ala	
120 125 130	
aca ctt cgt gtt tat aag cca tca gct gga aac aat tcc ctc tat cgg	535
Thr Leu Arg Val Tyr Lys Pro Ser Ala Gly Asn Asn Ser Leu Tyr Arg	
135 140 145	
gac aca gca gtt ttt gaa tgt ttg cca caa cat gcg atg ttt gga aat	583
Asp Thr Ala Val Phe Glu Cys Leu Pro Gln His Ala Met Phe Gly Asn	
150 155 160 165	
gat aca att acc tgc acg aca cat gga aat tgg act aaa tta cca gaa	631
Asp Thr Ile Thr Cys Thr Thr His Gly Asn Trp Thr Lys Leu Pro Glu	
170 175 180	
tgc agg gaa gta aaa tgc cca ttc cca tca aga cca gac aat gga ttt	679
Cys Arg Glu Val Lys Cys Pro Phe Pro Ser Arg Pro Asp Asn Gly Phe	
185 190 195	
gtg aac tat cct gca aaa cca aca ctt tat tac aag gat aaa gcc aca	727
Val Asn Tyr Pro Ala Lys Pro Thr Leu Tyr Tyr Lys Asp Lys Ala Thr	
200 205 210	
ttt ggc tgc cat gat gga tat tct ctg gat ggc ccg gaa gaa ata gaa	775



Phe Gly Cys His Asp Gly Tyr Ser Leu Asp Gly Pro Glu Glu Ile Glu  
 215 220 225  
 tgt acc aaa ctg gga aac tgg tct gcc atg cca agt tgt aaa gca tct 823  
 Cys Thr Lys Leu Gly Asn Trp Ser Ala Met Pro Ser Cys Lys Ala Ser  
 230 235 240 245  
 tgt aaa gta cct gtg aaa aaa gcc act gtg gtg tac caa gga gag aga 871  
 Cys Lys Val Pro Val Lys Lys Ala Thr Val Val Tyr Gln Gly Glu Arg  
 250 255 260  
 gta aag att cag gaa aaa ttt aag aat gga atg cta cat ggt gat aaa 919  
 Val Lys Ile Gln Glu Lys Phe Lys Asn Gly Met Leu His Gly Asp Lys  
 265 270 275  
 gtt tct ttc ttc tgc aaa aat aag gaa aag aag tgt agc tat aca gag 967  
 Val Ser Phe Phe Cys Lys Asn Lys Glu Lys Lys Cys Ser Tyr Thr Glu  
 280 285 290  
 gat gct cag tgt ata gat ggc act atc gaa gtc ccc aaa tgc ttc aag 1015  
 Asp Ala Gln Cys Ile Asp Gly Thr Ile Glu Val Pro Lys Cys Phe Lys  
 295 300 305  
 gaa cac agt tct ctg gct ttt tgg aaa act gat gca tcc gat gta aag 1063  
 Glu His Ser Ser Leu Ala Phe Trp Lys Thr Asp Ala Ser Asp Val Lys  
 310 315 320 325  
 cca tgc taaggtggtt ttcagattcc acataaaaatg tcacacttgt ttcttgttca 1119  
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 aaaaaaaaa 1187

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 <212> PRT  
 <213> Homo sapiens

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 Thr Val Val Pro Leu Lys Thr Phe Tyr Glu Pro Gly Glu Glu Ile Thr  
 15 20 25  
 Tyr Ser Cys Lys Pro Gly Tyr Val Ser Arg Gly Gly Met Arg Lys Phe  
 30 35 40 45  
 Ile Cys Pro Leu Thr Gly Leu Trp Leu Ile Asn Thr Leu Lys Cys Thr  
 50 55 60  
 Pro Arg Val Cys Pro Phe Ala Gly Ile Leu Glu Asn Gly Ala Val Arg  
 65 70 75  
 Tyr Thr Thr Phe Glu Tyr Pro Asn Thr Ile Ser Phe Ser Cys Asn Thr  
 80 85 90  
 Gly Phe Tyr Leu Asn Gly Ala Asp Ser Ala Lys Cys Thr Glu Glu Gly  
 95 100 105  
 Lys Trp Ser Pro Glu Leu Pro Val Cys Ala Pro Ile Ile Cys Pro Pro  
 110 115 120 125  
 Pro Ser Ile Pro Thr Phe Ala Thr Leu Arg Val Tyr Lys Pro Ser Ala  
 130 135 140  
 Gly Asn Asn Ser Leu Tyr Arg Asp Thr Ala Val Phe Glu Cys Leu Pro  
 145 150 155  
 Gln His Ala Met Phe Gly Asn Asp Thr Ile Thr Cys Thr Thr His Gly  
 160 165 170  
 Asn Trp Thr Lys Leu Pro Glu Cys Arg Glu Val Lys Cys Pro Phe Pro  
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 Ser Arg Pro Asp Asn Gly Phe Val Asn Tyr Pro Ala Lys Pro Thr Leu  
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98

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																	963
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																	1059
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																	1299
																	1347



Phe Arg Leu Arg Gly Ile Lys Ala Gln Val Ala Leu Arg Leu Ala Glu  
 370 375 380  
 Leu Ala Arg Arg Gln Arg Arg Arg Gln Ala Arg Arg Glu Ala Glu Ala  
 385 390 395 400  
 Asp Lys Pro Arg Arg Leu Gly Arg Leu Lys Tyr Gln Ala Pro Asp Ile  
 405 410 415  
 Asp Val Gln Leu Ser Ser Glu Leu Thr Asp Ser Leu Arg Thr Leu Lys  
 420 425 430  
 Pro Glu Gly Asn Ile Leu Arg Asp Arg Phe Lys Ser Phe Gln Arg Arg  
 435 440 445  
 Asn Met Ile Glu Pro Arg Glu Arg Ala Lys Phe Lys Arg Lys Tyr Lys  
 450 455 460  
 Val Lys Leu Val Glu Lys Arg Ala Phe Arg Glu Ile Gln Leu  
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 Met Cys Leu Leu Leu Ser Cys  
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 cct tgc cac ccc tct gcc cac gga cag tcc atg tgg att gag aga acc 163  
 Pro Cys His Pro Ser Ala His Gly Gln Ser Met Trp Ile Glu Arg Thr  
 -5 1 5  
 tcc ttc gtg act gca tac aag ctg ccg ggg atc ctg cgc tgg ttt gag 211  
 Ser Phe Val Thr Ala Tyr Lys Leu Pro Gly Ile Leu Arg Trp Phe Glu  
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 gtg gtg cac atg tcg cag acc aca att agt cct ctg gag aat gcc ata 259  
 Val Val His Met Ser Gln Thr Thr Ile Ser Pro Leu Glu Asn Ala Ile  
 30 35 40  
 gaa acc atg tcc acg gcc aat gag aag atc ctg atg atg ata aac cag 307  
 Glu Thr Met Ser Thr Ala Asn Glu Lys Ile Leu Met Met Ile Asn Gln  
 45 50 55  
 tac cag agt gat gag acc ctc ccc atc aac cca ctc tcc atg ctc ctg 355  
 Tyr Gln Ser Asp Glu Thr Leu Pro Ile Asn Pro Leu Ser Met Leu Leu  
 60 65 70  
 aac ggg att gtg gac cct gct gtc atg gga ggc ttc gcc aag tat gag 403  
 Asn Gly Ile Val Asp Pro Ala Val Met Gly Gly Phe Ala Lys Tyr Glu  
 75 80 85

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Lys	Ala	Phe	Phe	Thr	Glu	Glu	Tyr	Val	Arg	Asp	His	Pro	Glu	Asp	Gln
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gac	aag	ctg	acc	cac	ctc	aag	gac	ctg	att	gca	tgg	cag	atc	ccc	ttc
Asp	Lys	Leu	Thr	His	Leu	Lys	Asp	Leu	Ile	Ala	Trp	Gln	Ile	Pro	Phe
				110					115					120	
ttg	gga	gct	ggg	att	aag	atc	cat	gag	aaa	agg	gtg	tca	gat	aac	ttg
Leu	Gly	Ala	Gly	Ile	Lys	Ile	His	Glu	Lys	Arg	Val	Ser	Asp	Asn	Leu
			125					130					135		
cga	ccc	ttc	cat	gac	cgg	atg	gag	gaa	tgt	ttc	aag	aac	ctg	aaa	atg
Arg	Pro	Phe	His	Asp	Arg	Met	Glu	Glu	Cys	Phe	Lys	Asn	Leu	Lys	Met
		140					145				150				
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Lys	Val	Glu	Lys	Glu	Tyr	Gly	Val	Arg	Glu	Met	Pro	Asp	Phe	Asp	Asp
	155					160					165				
agg	aga	gtg	ggc	cgt	ccc	agg	tct	atg	ctg	cgc	tca	tac	aga	cag	atg
Arg	Arg	Val	Gly	Arg	Pro	Arg	Ser	Met	Leu	Arg	Ser	Tyr	Arg	Gln	Met
170				175						180					185
tcc	atc	atc	tct	ctg	gct	tcc	atg	aat	tct	gac	tgc	agc	acc	ccc	agc
Ser	Ile	Ile	Ser	Leu	Ala	Ser	Met	Asn	Ser	Asp	Cys	Ser	Thr	Pro	Ser
			190					195						200	
aag	cct	acc	tca	gag	agc	ttt	gac	ctg	gaa	tta	gca	tca	ccc	aag	acg
Lys	Pro	Thr	Ser	Glu	Ser	Phe	Asp	Leu	Glu	Leu	Ala	Ser	Pro	Lys	Thr
			205				210						215		
ccg	aga	gtg	gag	cag	gag	gaa	ccg	atc	tcc	ccg	ggg	agc	acc	ctg	cct
Pro	Arg	Val	Glu	Gln	Glu	Glu	Pro	Ile	Ser	Pro	Gly	Ser	Thr	Leu	Pro
		220				225						230			
gag	gtc	aag	ctg	cgg	agg	tcc	aag	aag	agg	aca	aag	aga	agc	agc	gta
Glu	Val	Lys	Leu	Arg	Arg	Ser	Lys	Lys	Arg	Thr	Lys	Arg	Ser	Ser	Val
	235					240					245				
gtt	ttt	gcg	gat	gag	aaa	gca	gct	gca	gag	tcg	gac	ctg	aag	cgg	ctt
Val	Phe	Ala	Asp	Glu	Lys	Ala	Ala	Ala	Glu	Ser	Asp	Leu	Lys	Arg	Leu
250				255						260					265
tcc	agg	aag	cat	gag	ttc	atg	agt	gac	acc	aac	ctc	tcg	gag	cat	gcg
Ser	Arg	Lys	His	Glu	Phe	Met	Ser	Asp	Thr	Asn	Leu	Ser	Glu	His	Ala
			270					275						280	
gcc	atc	ccc	ctc	aag	gcg	tct	gtc	ctc	tct	caa	atg	agc	ttt	gcc	agc
Ala	Ile	Pro	Leu	Lys	Ala	Ser	Val	Leu	Ser	Gln	Met	Ser	Phe	Ala	Ser
			285					290					295		
cag	tcc	atg	cct	acc	atc	cca	gcc	ctg	gcg	ctc	tca	gtg	gca	ggc	atc
Gln	Ser	Met	Pro	Thr	Ile	Pro	Ala	Leu	Ala	Leu	Ser	Val	Ala	Gly	Ile
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 <212> PRT  
 <213> Homo sapiens

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 Gly Ile Leu Arg Trp Phe Glu Val Val His Met Ser Gln Thr Thr Ile  
 20 25 30  
 Ser Pro Leu Glu Asn Ala Ile Glu Thr Met Ser Thr Ala Asn Glu Lys  
 35 40 45  
 Ile Leu Met Met Ile Asn Gln Tyr Gln Ser Asp Glu Thr Leu Pro Ile  
 50 55 60 65  
 Asn Pro Leu Ser Met Leu Leu Asn Gly Ile Val Asp Pro Ala Val Met  
 70 75 80  
 Gly Gly Phe Ala Lys Tyr Glu Lys Ala Phe Phe Thr Glu Glu Tyr Val  
 85 90 95  
 Arg Asp His Pro Glu Asp Gln Asp Lys Leu Thr His Leu Lys Asp Leu  
 100 105 110  
 Ile Ala Trp Gln Ile Pro Phe Leu Gly Ala Gly Ile Lys Ile His Glu  
 115 120 125  
 Lys Arg Val Ser Asp Asn Leu Arg Pro Phe His Asp Arg Met Glu Glu  
 130 135 140 145  
 Cys Phe Lys Asn Leu Lys Met Lys Val Glu Lys Glu Tyr Gly Val Arg  
 150 155 160  
 Glu Met Pro Asp Phe Asp Asp Arg Arg Val Gly Arg Pro Arg Ser Met  
 165 170 175  
 Leu Arg Ser Tyr Arg Gln Met Ser Ile Ile Ser Leu Ala Ser Met Asn  
 180 185 190  
 Ser Asp Cys Ser Thr Pro Ser Lys Pro Thr Ser Glu Ser Phe Asp Leu  
 195 200 205  
 Glu Leu Ala Ser Pro Lys Thr Pro Arg Val Glu Gln Glu Glu Pro Ile  
 210 215 220 225  
 Ser Pro Gly Ser Thr Leu Pro Glu Val Lys Leu Arg Arg Ser Lys Lys  
 230 235 240  
 Arg Thr Lys Arg Ser Ser Val Val Phe Ala Asp Glu Lys Ala Ala Ala  
 245 250 255  
 Glu Ser Asp Leu Lys Arg Leu Ser Arg Lys His Glu Phe Met Ser Asp  
 260 265 270  
 Thr Asn Leu Ser Glu His Ala Ala Ile Pro Leu Lys Ala Ser Val Leu  
 275 280 285  
 Ser Gln Met Ser Phe Ala Ser Gln Ser Met Pro Thr Ile Pro Ala Leu  
 290 295 300 305  
 Ala Leu Ser Val Ala Gly Ile Pro Gly Leu Asp Glu Ala Asn Thr Ser  
 310 315 320  
 Pro Arg Leu Ser Gln Thr Phe Leu Gln Leu Ser Asp Gly Asp Lys Lys  
 325 330 335  
 Thr Leu Thr Arg Lys Lys Val Asn Gln Phe Phe Lys Thr Met Leu Ala  
 340 345 350  
 Ser Lys Ser Ala Glu Glu Gly Lys Gln Ile Pro Asp Ser Leu Ser Thr  
 355 360 365  
 Asp Leu  
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<220>  
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 Met Ser Thr Phe  
 1  
 ttc tcg gac aca gca tgg atc tgc ctg gct gtc ccc aca gta cta tgt 162  
 Phe Ser Asp Thr Ala Trp Ile Cys Leu Ala Val Pro Thr Val Leu Cys  
 5 10 15 20  
 ggg aca gta ttt tgc aaa tac aag aag agc tca ggg cag ctg tgg agc 210  
 Gly Thr Val Phe Cys Lys Tyr Lys Lys Ser Ser Gly Gln Leu Trp Ser  
 25 30 35  
 tgg atg gtc tgc ctg gca ggc ctc tgt gca gtc tgc ctg ctc atc ctg 258  
 Trp Met Val Cys Leu Ala Gly Leu Cys Ala Val Cys Leu Leu Ile Leu  
 40 45 50  
 tcc cct ttt tgg ggc ttg atc ctc ttc tcg gtg tca tgc ttc ctc atg 306  
 Ser Pro Phe Trp Gly Leu Ile Leu Phe Ser Val Ser Cys Phe Leu Met  
 55 60 65  
 tat act tac tta tct ggc caa gaa ttg tta cct gtg gat cag aag gca 354  
 Tyr Thr Tyr Leu Ser Gly Gln Glu Leu Leu Pro Val Asp Gln Lys Ala  
 70 75 80  
 gtc ctg gtg aca ggt ggt gat tgc ggg ctt ggc cat gct ttg tgc aag 402  
 Val Leu Val Thr Gly Gly Asp Cys Gly Leu Gly His Ala Leu Cys Lys  
 85 90 95 100  
 tat ctg gat gag ctg ggc ttc acg gta ttt gcc gga gtt ttg aat gaa 450  
 Tyr Leu Asp Glu Leu Gly Phe Thr Val Phe Ala Gly Val Leu Asn Glu  
 105 110 115  
 aat ggc cca gga gct gag gaa ttg cga aga acc tgc tct ccg cgc ctc 498  
 Asn Gly Pro Gly Ala Glu Glu Leu Arg Arg Thr Cys Ser Pro Arg Leu  
 120 125 130  
 tcg gtg ctc caa atg gac atc acg aag cca gtg cag ata aaa gat gct 546  
 Ser Val Leu Gln Met Asp Ile Thr Lys Pro Val Gln Ile Lys Asp Ala  
 135 140 145  
 tac agc aag gtt gca gca atg ctg cag gac aga gga ctg tgg gct gtg 594  
 Tyr Ser Lys Val Ala Ala Met Leu Gln Asp Arg Gly Leu Trp Ala Val  
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 Ile Asn Asn Ala Gly Val Leu Gly Phe Pro Thr Asp Gly Glu Leu Leu  
 165 170 175 180  
 ctt atg act gac tac aaa caa tgc atg gcc gtg aac ttc ttt gga act 690





FO90300 CHEM600

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Ser Pro Arg Leu Ser Val Leu Gln Met Asp Ile Thr Lys Pro Val Gln		
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Ile Lys Asp Ala Tyr Ser Lys Val Ala Ala Met Leu Gln Asp Arg Gly		
145	150	155
Leu Trp Ala Val Ile Asn Asn Ala Gly Val Leu Gly Phe Pro Thr Asp		
165	170	175
Gly Glu Leu Leu Met Thr Asp Tyr Lys Gln Cys Met Ala Val Asn		
180	185	190
Phe Phe Gly Thr Val Glu Val Thr Lys Thr Phe Leu Pro Leu Leu Arg		
195	200	205
Lys Ser Lys Gly Arg Leu Val Asn Val Ser Ser Met Gly Gly Gly Ala		
210	215	220
Pro Val Glu Arg Leu Ala Ser Tyr Gly Ser Ser Lys Ala Ala Val Thr		
225	230	235
Met Phe Ser Ser Val Met Arg Leu Glu Leu Ser Lys Trp Gly Ile Lys		
245	250	255
Val Ala Ser Ile Gln Pro Gly Gly Phe Leu Thr Asn Ile Ala Gly Thr		
260	265	270
Ser Asp Lys Trp Glu Lys Leu Glu Lys Asp Ile Leu Asp His Leu Pro		
275	280	285
Ala Glu Val Gln Glu Asp Tyr Cys Gln Asp Tyr Ile Leu Ala Gln Arg		
290	295	300
Asn Phe Leu Leu Leu Ile Asn Ser Leu Ala Ser Lys Asp Phe Ser Pro		
305	310	315
Val Leu Arg Asp Ile Gln His Ala Ile Leu Ala Lys Ser Pro Phe Ala		
325	330	335
Tyr Tyr Thr Pro Gly Lys Gly Ala Tyr Leu Trp Ile Cys Leu Ala His		
340	345	350
Tyr Leu Pro Ile Gly Ile Tyr Asp Tyr Phe Ala Lys Arg His Phe Gly		
355	360	365
Gln Asp Lys Pro Met Pro Arg Ala Leu Arg Met Pro Asn Tyr Lys Lys		
370	375	380
Lys Ala Pro		
385		